Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- permanent accession numbers. The new UniProt record may not contain the previous temporary numbers from the most recent version of UniProt. These sequences have been assigned new Please note that the curators of the UniProt database have purged some temporary accession accession number.
- extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein If you encounter an accession number from an older search run against UniProt (results file Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

members of the public who may encounter UniProt temporary accession When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or numbers This Page Blank (uspic,



STIC-Biotech/ChemLib



From:

Bunner, Bridget

Sent:

Tuesday, February 21, 2006 3:47 PM

To:

STIC-Biotech/ChemLib

Subject:

sequence search

Hi! I'd like to request a sequence search for case 10/620,642:

- 1. the amino acid sequence of SEQ ID NO: 46
- 2. the amino acid sequence of SEQ ID NO: 61
- 3. the amino acid sequence of SEQ ID NO: 63

Thanks!

Bridget Bunner

Art Unit 1647 Rem 4C65 (571) 272-0881 mailbox 4C70

[130 2 1 ZM

EB 21 7m

Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed:
Searcher Prep Time:
Online Time:

Type of Search

NA#______ AA#:_____

S/L:_____Oligomer:_____

Encode/Transl:_____

Structure #:_____Text:___

Inventor:_____ Litigation:_____

Vendors and cost where applicable
STN:
DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Other (Specify):



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polypeptide(s) - for stimulating the growth of cells, esp. for treating disorders involving blood
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Aaw27607 |
Aay53284 |
Aab98356 |
Aab98367 |
Aab98367 |
Aab98415 |
Aab96942 |
Aab96942 |
Aab96952 |
Aab73566 |
Aab73566 |
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/label= sig_peptide
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90US-00537198.
90US-00573616.
90WO-US005548.
90US-00589701.
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N-PSDB; AAT04889.
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11-JUN-1990;
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28-SEP-1990;
01-OCT-1990;
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14-MAY-1996
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   Aar95175 Stem cell
Aab892586 Human ste
Aab865940 Human ste
Aab873565 Human SCF
Aau873565 Human SCF
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Aau87223 Human SCF
Ade22474 Human Ste
Ade24744 Human Ste
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                GenCore (c) 1993
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Post-processing:

Database

Title: Perfect score:

Sequence:

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OM protein

Run on:

Scoring table:

Searched:

Score

Result

WPI; 1996-251760/25

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    AAR83997 is human stem cell factor (SCF). Non-naturally occuring SCF and C-terminally truncated polypeptides stimualte growth of primitive progenitors such as haematopoletic progenitor cells, neural stem cells and primordial germ stem cells. The peptides can be used in a composition for treating leucopenia, anaemia or thrombocytopenia, for enhancing engraftment of bone marrow during transplantation or for bone marrow recovery after chemotherapy or radiation-induced bone marrow aplasia or myelosuppression. They can also be used for the treating neoplasia, nerve damage, infertility, intestinal damage or myelopoliferative disorders. Autibodies may be raised against the peptides for use in detection or neutralisation of SCF in serum. SCF may be useful for the treatment of AIDS and severe combined immunodeficiency (SCID) states alone or in combination with other factors such as IL-7. (Updated on 25-MAR-2003 to correct PF field.)
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/label= Mat_protein
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28-APR-1995;
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A DNA sequence (AAT29489) codes for human stem cell factor (SCF) (AAR95175). The full-length SCF transcript consists of 8 exons. A novel splice variant has been identified that appears to arise from the inclusion of a novel exon (see also AAT29488) between exons 3 and 4 of the gene. The resulting frameshift produces a novel SCF consisting of the first 39 amino acids of mature SCF followed by a 33-amino acids Cterminal region (AAR95174). The novel SCF is useful for ensuring correct development of pre-implantation embryos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                  Stem cell factor comprising C-terminal sequence given in specification useful to ensure correct development of pre-implantation embryos before
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28-SEP-1990;
01-OCT-1990;
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27-MAR-2001.
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                                                                                                                                                     Amethod has been developed of making haematopoietic cells suitable for administration to a subject. The method comprises: (a) obtaining the method comprises: (b) obtaining the cells haematopoietic progenitor cells from a donor; and (b) expanding the cells by adding to the cells a haematopoietically effective dose of a confirmation and one or more of the biological properties of naturally confirmation and one or more of the biological properties of naturally confirmation and one or more of the biological properties of naturally confirmation and one capable of maturing early haematopoietic progenitor cells including early haematopoietic progenitor cells which are capable of maturing to erythroid, megakaryocyte, can macrophage cells. SCF results in absolute increases in haematopoietic cells of both myeloid and lymphoid lineages. SCF is useful for treating haematopoietic disorders. The method is useful conformation bene matrow transplant. SCF is useful for enhancing the cefficiency of gene therapy based on transfecting haematopoietic stem cefficiency of gene therapy based on transfecting haematopoietic stem cefficiency of gene therapy based on transfecting haematopoietic recovery after acute bhood loss and as a boost to the immune system for fighting neoplasia (cancer). The present sequence represents a specifically confident human SCF from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
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                                                                             Production of hematopoietic cells suitable for administration to a subject using progenitor cells and expanding the cells using stem cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human stem celll factor (SCF) protein SEQ ID NO:46.
              Martin FH;
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                                                                                                                                  Claim 21; Fig 15C; 123pp; English.
              Bosselmann
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Best Local Similarity 100.
Matches 208; Conservative
            Suggs SV,
                                     WPI; 2000-259135/23.
N-PSDB; AAA13716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 208 AA;
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                                                                                                          factor.
              Zsebo
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cell,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 1061; DB 4 Best Local Similarity 100.0%; Pred. No. 2e-103; Matches 208; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                               Martin FH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 16; Fig 15C; 210pp; English.
                                                                                                                                                                                                                                                                                            Zsebo KM, Bosselman RA, Suggs
                                        89US-00422383.
90US-00537198.
90US-00573616.
90US-00589701.
92US-00172329.
95US-00449653.
98US-00224681
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                                                                                                                                                                                                                                                  (AMGE-) AMGEN INC.
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                                                                                                         01-OCT-1990;
25-NOV-1992;
21-DEC-1993;
24-MAY-1995;
31-DEC-1998;
                                          16-OCT-1989,
11-JUN-1990,
                                                                                         24-AUG-1990
                                                                                                                                                                                                        12-JAN-1998
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                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids encoding stem cell factor useful for treating disorders involving blood cells, e.g. leukemia, splenomegaly, Hodgkin's disease, Kala azar, anemia and septicemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly; anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder.
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                                                                                                                                                                                                                                                                                                                                     Suggs SV, Martin FH;
                                                                    1. 25
/label= Signal_peptide
26. 208
/label= Mature_SCF
                                                         cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Fig 15C; 209pp; English
                                                                                                                                                                                                    89US-00422383.
90US-00537198.
90US-00573616.
90US-00589701.
93US-00172329.
                                                                                                                                                                                95US-00482918
                                                                                                                                                                                                                                                                                                                                        Bosselman RA,
                                                                                                                                                                                                                                                                           (ZSEB/) ZSEBO K M.
(BOSS/) BOSSELMAN R A.
(SUGG/) SUGGS S V.
(MART/) MARTIN F H.
                                                                                                                                                                                                                                                                                                                                                             2001-298941/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 208 AA;
                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAS04121
                                     Homo sapiens
                                                                                                                                 US6207417-B1
                                                                                                                                                                                07-JUN-1995;
                                                                                                                                                                                                                                                      21-DEC-1993;
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01-OCT-1990;
                                                                                                                                                        27-MAR-2001
                                                                                                                                                                                                        16-OCT-1989;
                                                                                                                                                                                                                    11-JUN-1990
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                                                                    Peptide
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The present invention provides the protein and coding sequences of mammalian stem cell factors (SCFS). These are capable of stimulating the growth of early haematopoietic progenitor cells, neural stem cells and primordial germ stem cells. The sequences are useful in the treatment of leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal naemajubinuria, malaria, pigmentation disorders, neurological and intestinal damage, infertility, ALDS and severe combined immunodeficiency (SCID). The present sequence is an SCF described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated non-human mammalian stem cell factor polypeptide stimulating growth of early hematopoietic progenitor cells, useful for treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar, aarcoldosis.
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                                                                                                                                                                                                                                                                                                                                       Human; rat; mammal; stem cell factor; SCF; cell growth stimulation; gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia; neurological damage; intestinal damage; infertility; AIDS; SCID; severe combined immunodeficiency.
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100.0%; Pred. No. 2e-103;
iive 0; Mismatches 0;
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/label= signal_peptide
26. .208
/label= mature_stem_cell_factor
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181 KPFMLPPVAASSLRNDSSSSNSKYIYLI 208
                                                                                                                                                                                                                                                                                                   Human stem cell factor SEQ ID NO: 46.
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                                                                                                                                                 AAB96940 standard; protein; 208
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90US-00537198.
90US-00573616.
90US-00589701.
92US-00982255.
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Matches 208; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-353108/37.
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25-NOV-1992;
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Peptide
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splenomegaly, Kala azar, sarcoidosis, military tuberculosis, disseminated fungus disease, Fulminating septicaemia, malaria, vitamin B12 and folic acid deficiency, pyridoxine deficiency, and hypopigmentation disorders such as piebaldism and vitiligo
                                                                                                                                                                                                                                                                              121 KOLKKSPKSPEPRLFTPEEFPRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                               KOLKKSPKSPEPRLFTPBEFFRIFNRSIDAFKDFVVASBTSDCVVSSTLSPEKOSRVSVT 180
                                                                                                                                                                  1 MKKTQTWILITCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                         MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                                                                                                                                        61 MDVLPSHCWISEMVVQLSDSLTDLLDKRSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, stem cell factor, SCF, early haematopoietic progenitor cell;
blood disorder, leukaemia, Hodgkin's disease; lymphoma; splenomegaly;
anaemia, Kala azar, septicemia, malaria, hypopigmentation disorder.
                                                                                                                                                     1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated DNA sequence, encoding polypeptide product useful for stimulating growth of early hematopoietic progenitor cells.
                                                                                             100.0%; Score 1061; DB 4; Length 208; 100.0%; Pred. No. 2e-103; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human SCF (stem cell factor) protein encoded by SCF cDNA.
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/label= Signal_peptide
26. .208
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90US-00537198.
90US-00573616.
90US-00589701.
92US-00982255.
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                                                                                                            Local Similarity .vv. nes 208; Conservative
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N-PSDB; AAS04222.
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                                                                     Sequence 208 AA;
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01-OCT-1990;
25-NOV-1992;
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                                                                                               Query Match
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Matches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New stem cell factor polypeptides and their analogs which stimulate growth of early hematopoietic progenitors, useful for treating aplastic anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's
            Human, stem cell factor; SCF; early haematopoietic progenitor cell;
blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
anaemia; Kala azar; septicaemia; malaria; hypopigmentation disorder.
                                                                                                                                                                                                                                                                                                    Human SCF (stem cell factor) protein #2, encoded by SCF cDNA.
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/label= Signal_peptide
26. .208
/label= Mature_SCF
                                                                                                                       KPFMLPPVAASSLRNDSSSSNSKYIYLI
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                                                                                                                                                                                                                     AAB73565 standard; protein; 208
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90US-00537198.
90US-00573616.
90US-00589701.
91US-00684535.
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N-PSDB; AAH23899.
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24-AUG-1990;
01-OCT-1990;
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25-NOV-1992;
21-DEC-1993;
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                    encoded by SCF control of the present invention relates to novel from cell factors (AANU02761, AANU02775, AANU02797) and the polynucleotides encoding them. SCF stimulate primitive progenitor cells including early haematopoietic progenitor cells. The invention also describes SCF peptides (AANU02777-AANU02794) and the oligonucleotides of producing sCF sequences. The polynucleotide encoding SCF is useful for producing SCF and useful in such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia, congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis, disseminated fungus disease, Pulminating septicemia, malaria, vitamin B12 and folic acid deficiancy, pyridoxine deficiency, and hypopigmentation disorders such as piebaldism and vitiligo
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blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
hypopigmentation disorder; viral disorder; AIDS.
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           sequence represents human SCF (stem cell factor) protein
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                                                                                                                                                                                                                                   Query Match 100.0%; Score 1061; DB 4. Best Local Similarity 100.0%; Pred. No. 2e-103; Matches 208; Conservative 0; Mismatches 0
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/label= Mature_SCF
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90US-00573616.
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91US-00684535.
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                                                                                                                                                                                                               Sequence 208 AA;
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01-OCT-1990;
10-APR-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Increasing the number of early hematopoietic progenitor cells in the peripheral blood useful for the treatment of blood disorders including Hodgkin's disease comprises the administration of human stem cell factor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDXLVNIVDDLVECVKENSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKKTQTWILTCIYLQLLLFNPLVKTBGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; stem cell factor; SCF protein; leucopaenia; thrombocytopaenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1061; DB 4
100.0%; Pred. No. 2e-103;
Live 0; Mismatches 0
                                                                                                                                                                                                                                                                                                Martin FH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KPFMLPPVAASSLRNDSSSSNSKYIYLI 208
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                                                                                                                                                                                                                                                                                                   Suggs SV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Fig 15C; 210pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE22323 standard; protein; 208 AA
92US-00982255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                   Zsebo KM, Bosselman RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 208; Conservative
                                                                                                         (ZSEB/) ZSEBO K M.
(BOSS/) BOSSELMAN R A.
(SUGG/) SUGGS S V.
(MART/) MARTIN F H.
                                                                                                                                                                                                                                                                                                                                                                             2001-407312/43.
                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-407312
N-PSDB; AAS10457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 208 AA;
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121 KOLKKSFKSPEPRLFTPEEFPRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180

KPFMLPPVAASSLRNDSSSSNSKYIYLI 208 KPFMLPPVAASSLRNDSSSSNSKYIYLI 208

181 181 Ą

ABG95641 standard; protein; 208

ABG95641 ID ABG

KDLKKSFKSPEPRLFTPEEFFRI FNRSI DAFKDFVVASETSDCVVSSTLSPEKDSRVSVT

121

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The present invention relates to novel non-naturally-occurring stem cell factor (SCF) polypeptides having an amino acid sequence sufficiently comparative of that of naturally-occurring SCF to allow possession of haematopoietic biological activity of naturally occurring SCF. Sequences of the invention are useful for treating leucopaenia, thrombocytopaenia, anaemia and for enhancing bone marrow recovery in treatment of radiation, engraftment of bone marrow during transplantation in mammals and chemical or chemotherapeutic induced bone marrow aplasia or myelosuppression. They are also useful for treating acquired immune deficiency in a human, nerve damage, neoplasia, infertility, myeloproliferative disorder, intestinal chamage in a mammal. SCF sequences are useful for preparing biologically active polymer polypeptide adduct, for enhancing transfer of a gene into a mammal. They are useful for treating myelofibrosis, myelosclerosis, osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma, catecopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma, costeopetrosis, se disease, lymphoma, dalseaminated fungus disease, nalaria, military tuberculosis, Pulminating septicaemia, pyridoxine deficiency, vitamin B12 and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation of an disorders such as piebaldism, halds (armune deficiency syndrome) and sitting and military of disorders such as piebaldism, and prantic connection of an active propertices and folic acid deficiency, Diamond Blackfan anaemia, connections and military of humances.
acquired immune deficiency syndrome; malaria; military tuberculosis; pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency; Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel non-naturally-occurring stem cell factor polypeptide, useful treating leucopenia, thrombocytopenia, anemia and for enhancing engraftment of bone marrow during transplantation in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present sequence is human SCF protein
                                                                                                                                                                                                                /note= "Human mature SCF protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Martin FH;
                                                                                                                                                 1. .25
/label= Signal-peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Suggs SV,
                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 9; Fig 15C; 217pp; English
                                                                                                                                                                                                                                                                                                                                          98US-00005243
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                                                                                                                                                                                                                                                                                                                                                                                                                        (ZSEB/) ZSEBO K M.
(BOSS/) BOSSELMAN R A.
(SUGG/) SUGGS S V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002-350789/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                             (BOSS/) BOSSELMAN R
(SUGG/) SUGGS S V.
(MART/) MARTIN F H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and vitiligo. The
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                                                                                                                                                                                                                                                                                                                                          12-JAN-1998;
                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                  14-FEB-2002
                                                                                                                                             Peptide
                                                                                                                                                                                          Protein
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haematopoietic system; metastatic carcinoma; acute leukaemia; multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo; refractory erythroblastic anaemia; miliary tuberculosis; cytostatic; disseminated fungus disease; haematopoietic; tuberculostatic; antianaemic; antifungal; antimalarial; dermatological; human.

Stem cell factor; SCF; blood-forming system; blood cell disorder;

Human SCF protein sequence encoded by cDNA.

(first entry)

05-DEC-2002

ABG95641;

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polymicleotide sequences encoding the SCFs, and methods of producing polymicleotide sequences encoding the SCFs, and methods of producing them. SCFs are involved in the blood-forming (haematopoietic) system in mammals, particularly humans. The method of the invention is useful for the production of human SCF. The stem cell factors are useful to treat disorders involving blood cells e.g. metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, refractory erythroblastic anaemia, miliary tuberculosis, disseminated fungus disease, malaria, and vitiligo. The present sequence represents human SCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to novel grem cell factors (SCFs)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Production of a human stem cell factor (SCF) polypeptide for disorders involving blood cells, such as leukemia, comprises mammalian cells comprising non-human SCF promoter DNA linked encoding the human SCF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1061; DB 5;
100.0%; Pred. No. 2e-103;
tive 0; Mismatches 0;
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Matches 208; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2002-684093/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-684093/
N-PSDB; ABS73858.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECYKENSS 120
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100.0%; Pred. No. 2e-103;
ive 0; Mismatches 0
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Best Local Similarity 100.
Matches 208; Conservative
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treating culturing to DNA

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Martin

Bosselman RA,

Zsebo KM, Suggs SV,

(AMGE-) AMGEN INC.

01-OCT-1990; 04-OCT-1990; 04-OCT-1990;

89US-00422383. 90US-00537198. 90US-00573616. 90US-00589701. 90US-0010899.

04-OCT-1990; 2002EP-00008587

16-OCT-1989; 11-JUN-1990; 28-SEP-1990

18-SEP-2002,

Homo sapiens EP1241258-A2 ö

Gaps

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ADP99316 standard; protein; 208
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/note= "Mature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                              Local Similarity 100.
nes 208; Conservative
                                                                                                                                                      Sequence 208 AA;
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                                                                                                                           invention.
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Matches
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                                                                                                                           KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                           KOLKKSPKSPEPRLFTPEEPFRIFNRSIDAFKOFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                haematopoietic activity and the polynucleotides encoding them. The polypeptides are used for treating infertility, intestinal damage, myeloproliferative disorders, leucopenia, thrombocytopenia or anaemia, for improving engraftment of bone marrow transplants, for enhancing bone marrow recovery after radiotherapy or chemotherapy and in treatment of
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                                                                                                                                                                                                                                                                                                                                                                                            Human; stem cell factor; SCF; haematopoietic activity; infertility; intestinal damage; myeloproliferative disorder; leucopenia; thrombocytopenia; anaemia; bone marrow transplant; immune deficiency; neoplasia; nerve damage; osteoporosis; metastatic carcinoma; leukaemia; miliary tuberculosis; haematopoietic progenitor cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-natural stem cell factor, useful for treating e.g. leucopenia deficiency, also related nucleic acid and antibodies.
                             MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                      MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
             MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                    MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suggs SV, Martin FH;
                                                                                                                                                                                                                                                                                                                                                                  Human stem cell factor (SCF) polypeptide #2.
                                                                                                                                                                                                   KPFMLPPVAASSLRNDSSSSNSKYIYLI 208
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91US-00684535.
92US-00982255.
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90US-00573616.
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95US-00449653
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                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZSEBO K M.
BOSSELMAN R A.
SUGGS S V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-DEC-1998;
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(SUGG/) S
(MART/) N
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Human; SCF; stem cell factor; gene therapy;

M haematopoietic progenitor cell; aplastic anaemia;

M paroxysmal nocturnal haemoglobinuria; myelofibrosis; myelosclerosis;

M paroxysmal nocturnal haemoglobinuria; myelofibrosis; myelosclerosis;

M paroxysmal nocturnal laemoglobinuria; myelofibrosis; myelosclerosis;

M paroxysmal nocturnal laemoglobinuria; disease; Niemann-Pick disease;

M pidensi, n's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;

M pidensi, palenic pancytopaenis; miliary tuberculosis;

M primary splenic pancytopaenis; miliary tuberculosis;

M primary splenic pancytopaenis; miliary tuberculosis;

M primary splenic pancytopaenis; miliary tuberculosis;

M vitamin B12 deficiency; folic acid deficiency; pyridoxine deficiency;

M vitamin B12 deficiency; folic acid deficiency; pyridoxine deficiency;

M vitamin B12 deficiency; folic acid deficiency; pyridoxine deficiency;

M vitamin B12 demochaemis; hypopigmentation disorder; picbaldism;

W vitiligo; neurological damage; infertility; intestinal damage;

M irradiation; chemotherapy; AIDS; haematopoietic recovery;

M acute blood loss; neoplasm; cancer.
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immune deficiency, neoplasia, nerve damage, osteoporosis, metastatic carcinoma, leukaemia and miliary tuberculosis. The SCF polypeptides are also used to expand haematopoietic progenitor cells for transplantation and to prepare such cells for transfection with a gene. The SCF polynucleotides can be used for recombinant expression of the polypeptides and also as probes for mapping of the SCF gene, for identifying SCF-related diseases and as a marker for neighbouring genes. Antibodies raised against the polypeptides are useful in diagnosis and to remove SCF from blood. This sequence represents an SCF polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1061; DB 7,
100.0%; Pred. No. 2e-103;
ive 0; Mismatches 0;
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    .25
    /note= "Signal peptide"

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The invention relates to preparing a (vertebrate) human stem cell factor (SCF) polypeptide comprising growing host cells transformed or transfected with DNA encoding a human SCF that stimulates growth of haematopoietic progenitor cells under nutrient conditions, the DNA being operatively linked to an expression control sequence, and isolating the polypeptide produced. Also included is a recombinant host cell transformed or transfected with an expression control sequence, and isolating the polypeptide produced. Also included is a recombinant host cell comprising a vertebrate SCF polypeptide in the host cell. Disclosed as new are rat and human nuclet acids encoding SCF, SCF proteins from a number of other mammals and recombinantly expressed SCF protein fragments. The DNA mammals and recombinantly expressed SCF protein fragments. The DNA mammals and recombinant techniques or for generating new and useful variety of recombinant techniques or for generating new and useful variety of recombinant techniques or for generating new and useful cransfected prokaryotic and enkaryotic host cells, and new and useful methods for cultured growth of such host cells, and new and useful methods for cultured products. The DNA sequences are also useful as labelled probes in isolating human genomic DNA encoding SCF, in methods of production of SCF and SCF products are also useful as labelled probes in isolating human genetic therapy in humans and other mammals, and coperatively probes in solating human genetic therapy in humans and other mammals, and section in developing transgenic mammalian pecies which may serve as eukaryotic posterial sprinkesis. In genetic therapy in humans and other mammals, and assert of production of SCF and SCF products in quantity. The SCF is useful accordance and disease, lymphom, carefulom, vitamin but also useful for treating hematopoletic discoders, in genetic for production of scenario and place and as general carefular and propopiementation from irradiation or chemotherapy, and AIDS. SCF is also usefu
                                                                                                                                                                                                                                                                                                                                       Preparing a human stem cell factor (SCF) polypeptide, useful for treating hematopoietic disorders, e.g., aplastic anemia, comprises growing host cells transformed or transfected with DNA encoding a human SCF.
                                                                                                                                                                                                                                   Martin FH;
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 46; 210pp; English.
                                                                                                                                                                                                                                   Suggs SV,
89US-00422383.
90US-00537198.
90US-00589701.
91US-00684535.
92US-00192255.
93US-00172229.
                                                                                                                                                                                                                                 Zsebo KM, Bosselman RA,
                                                                                                                                                                                                                                                                            2004-497128/47.
                                                                                                                                                                                       (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                N-PSDB; ADP99315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 208 AA;
                                                                                   10-APR-1991;
                                                                                                      25-NOV-1992;
21-DEC-1993;
                                                                                                                                                24-MAY-1995;
                                             24-AUG-1990
                                                               01-OCT-1990
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ö MDVLPSHCWISEMVVQLSDSLTDLLDKPSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120 9 1 MKKTQTWILTCIYLQLLLENPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMILLKYVPG 1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS Gaps ; 0 DB 8; Length 208; Indels ö 100.0%; Score 1061; DB 8 100.0%; Pred. No. 2e-103; iive 0; Mismatches 0 Query Match Best Local Similarity 100. Matches 208; Conservative 61 61 요 셤 ઠ ò

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121 KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel stem cell factor (SCF) such as non-naturally-occurring SCF or naturally occurring SCF, useful for treating leukopenia, thrombocytopenia, anemia, and enhancing engraftment of bone marrow during transplantation.
                                                                                                                                                                                                                                                                                                      Human; stem cell factor; SCF; haematopoietic;
HT1080 fibrosarcoma cell line; 5637 bladder carcinoma cell line;
HC1080 fibrosarcoma cell line; 5637 bladder carcinoma cell line;
Lektopeania; thrombocytopenia; anaemia; bone marrow during transplant;
bone marrow aplasia; myelosuppression; immune deficiency; neoplasm;
nerve damage; infertility; intestinal damage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a stem cell factor (SCF) such as non-naturally-
occurring SCF having an amino acid sequence sufficiently duplicative of
that of naturally occurring SCF to allow possession of a haematopoietic
biological activity of naturally occurring stem cell factor, or naturally
occurring SCF. Also included are an isolated DNA sequence for use in
securing expression in a prokaryotic or eukaryotic host cell of non-
naturally occurring SCF, a prokaryotic or eukaryotic host cell
                                                                                                                                                                                                                                                                                                                                                                                           myeloproliferative disorder; early haematopoietic progenitor cell; haematopoictic disorders; aplastic anaemia; myelofibrosis; miner myelosclerosis; osteopetrosis; metastatic carcinoma; multiple myeloma; Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;
KOLKKSFKSPEPRLFTPREFFRIFNRSIDAFKOFVVASETSOCVVSSTLSPEKOSRVSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                            Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick di
Diamond-Blackfan anaemia; DBA; Fanconi's anaemia; gene therapy;
                                                                                                                                                                                                                                                                           Human stem cell factor, full length protein #1.
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                                                             KPFMLPPVAASSLRNDSSSSNSKYIYLI 208
                                                                                 181 KPFMLPPVAASSLRNDSSSSNSKYIYLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 9; SEQ ID NO 46; 216pp; English.
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                                                                                                                                                                             ADU50646 standard; protein; 208
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90US-00537198.
90US-00573616.
90US-00589701.
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2000US-00635249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUN-2002; 2002US-00175608
                                                                                                                                                                                                                                            13-JAN-2005 (first entry)
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BOSSELMAN R A.
SUGGS S V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acute blood loss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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07-JUN-1995;
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10-APR-1991
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121
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(BOSS/)
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transformed or transfected with the DNA, a polypeptide product of the expression of the DNA in a prokaryotic or eukaryotic host cell, an isolated DNA sequence coding for prokaryotic or eukaryotic host expression of non-naturally occurring SCF, a DNA sequence coding for a cypression of non-naturally occurring SCF, a DNA sequence coding for a polypeptide analogue of naturally-occurring stem cell factor, a biologically functional plasmid or viral DNA vector including the DNA sequence above, a prokaryotic or eukaryotic host cell factor, a biologically functional plasmid or viral DNA vector including the DNA sequence encoded by composite nucleic acid sequence atably transformed or transfected with the DNA, buman SCF CDNA obtained from #10.00 fibrosarcoma cell line or human SCF CDNA obtained from #10.00 fibrosarcoma cell line (and having one or more of in vitro biological carcinoma cell line, or human SCF CDNA obtained from #10.00 fibrosarcoma cell line (and having one or more of in vitro biological carcinoma cell line (and having one or more of in vitro biological carcinoma cell line (and having one or more of in vitro biological carcinoma cell line (and having one or more of in vitro biological carcinoma cell vitro biological carcinoma cell line (and having one or more of in vitro biological carcinoma cell vitrospecially occurring stem cell factor, and an antibody (Ab) specifically binding SCF. SCF. SCF is useful encoded transplantation in a mammal. SCF is useful for treating partients with therapeutically effective doses of SCF. SCF is useful for transfecting early haematopolitic progenitor cells with a gene to mammal which involves culturing early haematopoletic progenitor cells with a gene cultured cells with a gene. SCF is useful for transfecting the cultured cells with a gene. SCF is useful for transfecting the cultured cells with a gene. SCF is useful for transfecting the cultured cells with a gene. SCF is useful for transfecting agene to a mammal which involves culturing early haematopoletic progenitor cells

Sequence 208 AA;

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                                                                                                                                 61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                    61 MDVLPSHCWISEMYVQLSDSLTDLLDKFSNISBGLSNYSIIDKLVNIVDDLVBCVKENSS 120
                                                                                                                                                                                                     KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                       1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                                                    1 MKKTQTWILICIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                    Gaps
                                 .;
Query Match 100.0%; Score 1061; DB 8; Length 208; Best Local Similarity 100.0%; Pred. No. 2e-103; Matches 208; Conservative 0; Mismatches 0; Indels 0.
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Antianemic; Antiemetic; Cytostatic; Anti-HIV; Cardiovascular-Gen.; CNS-Gen.; Antibacterial; Immunosuppressive; Antibilinflammatory; Fungicide; Antiertility; ADDS; aplastic anemia; paroxysmal nocturnal hemoglobinuria; osteoperrosis; acute leukemia; multiple myeloma; hodgkins disease; lymphoma; gauchers disease;
                                                                                                   Human Stem Cell Factor, SEQ ID 46.
                                                                  (first entry)
                                                                    21-APR-2005
                                  ADW93091;
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ADW93091 standard; protein; 208 AA

RESULT 15

Stimulating proliferation of melanocyte cells in human, involves administering stem cell factor polypeptide or its biologically active fragments stimulating growth of melanocyte cells, and optionally carrier, to human. niemann pick disease; sarcoidosis; plasmodium infection; vitamin deficiency; hypopigmentation; vitiligo; infertility; chronic myelocytic leukemia; cell proliferation; Stem Cell R Suggs SV, Martin FH; 1. .25
/label= Signal_peptide /label= Mature_protein Location/Qualifiers 89US-00422383. 90US-00537198. 90US-00573616. 90US-00589701. 91US-00684535. 92US-00982255. 93US-00172229. 26-JUN-2000; 2000US-00604325 Zsebo KM, Bosselman RA, .208 WPI; 2005-160562/17. (AMGE-) AMGEN INC. N-PSDB; ADW93090 24-AUG-1990; 01-OCT-1990; 10-APR-1991; 25-NOV-1992; 21-DEC-1993; Homo sapiens US6852313-B1 24-MAY-1995; 08-FEB-2005 16-0CT-1989 11-JUN-1990 Peptide Protein Key

The present invention relates to a method (MI) for stimulating proliferation of melanocyte cells in a human. (MI) involves administering a Stem Cell Factor (SCF) protein, or its biologically active fragments that stimulates growth of melanocyte cells, and optionally a carrier, to the tsimulates growth of melanocyte cells, and optionally a carrier, to the human. The SCF is covalently conjugated to a water soluble polymer compensation of the script is covalently conjugated to a water soluble polymer of the more operations and proposition of the script is covalently conjugated to a water soluble polymer compensation and searly hematopoidetic progenitor cells that are capable of maturing to erythroid, megakaryocyte, granulocyte, are capable of maturing to erythroid, megakaryocyte, granulocyte, crimma macrophage cells, and non-hematopoidetic stem cells such as neural stem cells and primordial germ stem cells. (MI) is useful in accelerating bone marrow regeneration, and in augmenting T cell accelerating bone marrow regeneration, and in augmenting T cell accelerating bone marrow regeneration, and in augmenting T cell accelerating bone marrows regeneration, and in engandary are characterized by a reduction in functional marrow mass due to toxic, radiant or immunological injury. (MI) is useful in treating AlbS, aplacterized by a reduction in functional marrow mass due to toxic, radiant or immunological injury. (MI) is useful in treating Albacase, nultiple myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease, congestive splenomegaly, Kalazar, sarcoidosis, primary complexical disease, in disease, lymphoma, Gaucher's disease, intestinal damage resulting from irradiation or chemotherapy, and stem cell myeloproliferative disorders such as chronic myelogenous leukemia, configured in a syngeneic, allogeneic or autologous configured in earrow transplantation, and in enhancing the efficacy of gene configured and accelerate the invention. Claim 2; SEQ ID NO 46; 212pp; English.

Sequence 208 AA;

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        Query Match
        100.0%; Score 1061; DB 9; Length 208;

        Best Local Similarity 100.0%; Pred. No. 2e-103;

        Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

        Qy
        1 MKXTQTWILLTCIYLQLLENPLVKTEGICRNRVTRNVKOVTKLVANLPKOYMITLKYVPG 60

        Db
        1 MKXTQTWILLTCIYLQLLENPLVKTEGICRNRVTRNVKOVTKLVANLPROYMITLKYVPG 60

        Qy
        61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120

        Db
        61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120

        Qy
        121 KDLKKSFKSPEPRLFTPERFFRIPNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180

        Db
        121 KDLKKSFKSPERLFTPREFFRIPNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180

        Qy
        181 KPPMLPPVAASSLRNDSSSSNSKYIYLI 208

        Db
        181 KPPMLPPVAASSLRNDSSSSNSKYIYLI 208
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Search completed: February 22, 2006, 18:12:59 Job time : 125.336 secs

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OM protein - protein search, using sw model

February 22, 2006, 18:13:23; Search time 17.1901 Seconds (without alignments) 1164.223 Million cell updates/sec Run on:

Title: Perfect score:

US-10-620-642-46 1061 1 MKKTQTWILTCIYLQLLLFN......AASSLRNDSSSSNSKXIYLI 208 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

283416

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Regult No.	Score	Query Match	Length	DB	ID	Description
	1030	97.1	! ! !	7	A35974	mast cell growth f
7	899.5	84.8	274	~	I46575	c-kit ligand - pig
٣	890	83.9		~	B61190	mast cell growth f
4	886.5	83.6		N	847571	_
2	885.5	83.5		N	S58313	-
9	862.5	81.3		~	146929	l factor
7	857	80.8		~	B35974	Н
80	855	80.6	273	0	865801	cell
6	715	67.4	245	N	A37934	mast cell growth f
10	576.5	54.3	124	N	S29052	cell
11	570.5	53.8	287	N	870366	_
12	562.5	53.0	287	~	JN0637	stem cell factor p
13	479.5	45.2	253	~	S70367	cell
14	175.5	16.5	51	~	B35971	
15	172.5	16.3	49	N	A35971	mast cell growth f
16	97.5	9.5	1490	N	T16086	
17	97	9.1	1447	~	F82909	
18	94	8.9	1293	~	T27886	
19	94	8.9	1813	~	T19295	hypothetical prote
20	92.5	8.7	164	N	B69616	ㅁ
21	92.5	8.7	512	N	G86773	citrate (pro-38)-1
22	92	8.7	935	N	863261	SEC21 protein - ye
23	91	8.6	1107	~	861667	rar
24	90.5	8.5	616	7	A69136	ATP-dependent Clp
22	89	8.4	1734	7	A41101	4
26	88.5	•	545	7	B44054	orf2 protein - Jun
27	88.5	8.3	941	7	H84855	phosphoenolpyruvat
28	88	8.3	335	~	S44922	K18 antigen - Enta
29	88	8.3	465	0	H97165	flagellar hook-len

membrane-associate	DNA-directed RNA p	probable protein k	phosphoenolpyruvat	hypothetical prote	hypothetical prote	protein F28J9.3 (i	BRO1 protein - yea	hypothetical prote	molybdenum ABC tra	threonine synthase	hypothetical prote	hypothetical prote	hypothetical prote	probable protein k	merozoite surface
F97352	T31670	T04005	826235	T16411	T19850	F86486	S61104	T08607	A64579	G86887	T22794	T19493	T29762	B86461	A45949
8	~	7	N	~	~	N	~	~	Н	~	N	~	~	7	~
702	1690	649	996	664	246	436	844	1271	246	496	99	1334	222	614	636
8.3	8.3	8.2	8.3	8.2	8.2	8.2	8.3	8.2	8.1	8.1	8.1	8.1	8.1	8.1	8.1
88	88	87.5	87.5	87	86.5	86.5	86.5	86.5	98	98	98	98	85.5	85.5	85.5
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

A35974

Mast cell growth factor precursor - human
NyAlternate names: kit ligand; stem cell factor
C;Species: Homo sapiens (man)
C;Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 09-Jul-2004
C;Accession: A35974; A61190
R;Martin, F.H.; Suggs, S.V.; Langley, K.E.; Lu, H.S.; Ting, J.; Okino, K.H.; Morris, C. S. J. J.; Patel, A.C.; Fisher, B.P.; Erjavec, H.O.; Herrera, C.J.; Wypych, J.; Sachdev,...
Cell 63, 203-211, 1990
A;Title: Primary structure and functional expression of rat and human stem cell factor in A;Reference number: A35974; MUID:91004219; PMID:2208279

A; Molecule type: mRNA A; Residues: 1-273 < MAR.> A; Residues: 1-273 < MAR.> A; Cross-references: UNIPROT: P21583; UNIPARC: UP1000002D482; GB: M59964; NID: g337933; PIDN B; Anderson, D.M.; Williams, D.E.; Tuchinski, R.; Gimpel, S.; Eisenman, J.; Cannizzaro, I Cell Growth Differ. 2, 373-378, 1991 A; Title: Alternate splicing of mRNAs encoding human mast cell growth factor and localiz A; Reference number: A61190; MUID: 92172791; PMID: 1724381

A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-273 <AND>
A;Residues: 1-273 <AND>
A;Cross-references: UNIPARC:UPI00002D482

C,Genetics: A,Gene: GDB:MGF A,Cross-references: GDB:128026; OMIM:184745

A, Map position: 1242-12422
C; Superfamily: mouse mast cell growth factor
F; 1-25; Domain: signal sequence #status predicted <SIG>
F; 26-273; Product: mast cell growth factor #status predicted <MGS>
F; 26-189; Product: (or 26-100) mast cell growth factor, soluble form #status predicted <?
F; 215-237; Domain: transmembrane #status predicted <TWM>
F; 215-237; Domain: transmembrane #status predicted <TWM>
F; 210-237; Domain: transmembrane #status predicted

ö Gaps ö 97.1%; Score 1030; DB 2; Length 273; 99.5%; Pred. No. 4.2e-74; trive 0; Mismatches 1; Indels Matches 202; Conservative Query Match Best Local Similarity

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KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180 121

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A;Residues: 1-274 <ZHO>
A;Cross-references: UNIPROT:Q28132; UNIPARC:UPI0000135639; EMBL:D28934; NID:g538520; PIC
C;Superfamily: mouse mast cell growth factor
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C;Superfamily: mouse mast cell growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       stem cell factor, longer isoform - bovine
c;Species: Bos primispenius taurus (cattle)
C;Species: Bos primispenius taurus (cattle)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C;Accession: 847571
R;Zhou, J.H.; Hikono, H.; Ohtaki, M.; Kubota, T.; Sakurai, M.
Bjochim. Biophys. Acta 1223, 148-150, 1994
A;Title: Cloning and characterization of CDNAs encoding two normal isoforms of bovine 8
A;Reference number: 847571; MUID:94339176; PMID:7520283
A;Accession: 847571
A;Status: preliminary
A;Molecule type: mRMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        stem cell factor precursor - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: S58313
R;McInnes, C.J.; Logan, M.; Falconer, V.M.; Rawlins, P.; Huntly, J.; Haig, D.
S;McInnes, C.D.; Bobert Data Library, August 1995
B;Description: Molecular cloning and biological activity of ovine stem cell factor.
A;Reference number: S58313
                                                                                                                                                                                                                                                                 61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                         1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                               121 KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKOFVVASETSDCVVSSTLSPEK 173
                                                                                                                                                                                                                                                                                                                                                                     KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEK 173
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85.3%; Pred. No. 9.1e-63;
iive 16; Mismatches 13
Mismatches
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   Conservative
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A; Molecule type: mRNA
A; Residues: 1-202 <MCI>
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   173;
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N;Alternate names: kit ligand, short form; stem cell factor, short form

C;Date: O3-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004

C;Accession: B61190

C;Accession: B61190

R;Anderson, D.M.; Williams, D.E.; Tushinski, R.; Gimpel, S.; Bisenman, J.; Cannizzaro, I.

Cell Growth Differ. 2, 373-378, 1991

A;Title: Alternate splicing of mRNAs encoding human mast cell growth factor and localiza

A;Accession: B61190

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

A;Accession: B61190

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

A;Accession: B61190

A;Cross-references: UNIPROT:P21583; UNIPARC:UP1000002B351

C;Comment: Alternative splicing produces this short form in which a predicted cleavage s

C;Genetics:
A;Genetics: GDB:128026; OMIM:184745

A;Cross-references: GDB:128026; OMIM:184745

A;Cross-references: GDB:128026; OMIM:184745

A;Genetics: alternative splicing; glycoprotein; transmembrane protein

C;Genetics: alternative splicing; glycoprotein; cransmembrane protein

F;1-25/Domain: signal sequence #status predicted crans

E;90,97,118,145/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: UNIPROT: Q29030, UNIPARC: UPI0000135640; GB: L07786; NID: 9164420; PIDN
                                                                                                                                                                                                                                                                                                c-kit ligand - pig

Cispecies: Sus acrofe domestica (domestic pig)

Cispecies: Sus acrofe domestical domestic domestical domest
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84.8%; Score 899.5; DB 2; Length
Best Local Similarity 86.3%; Pred. No. 8.5e-64;
Matches 176; Conservative 17; Mismatches 10; Indels
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100.0%; Pred. No. 4.2e-63;
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Indels

Length 245;

Query Match Best Local Similarity

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mast cell growth factor - mouse

NyAlternate names: hematopoietic growth factor KL; ligand steel factor; stem cell factor

C;Species Mus musculus (house mouse)

C;Decies Mus musculus (house mouse)

C;Date: 28-Oct-1996 #sequence revision 27-Feb-1997 #text change 09-Jul-2004

C;Accession: S65801; A43751; A35976; A35972; A35975; A35973; I48768

R;Bedell, M.A.; Copeland, N.G.; Jenkins, N.A.

Genetics 142, 927-934, 1996

A;Title: Multiple pathways for Steel regulation suggested by genomic and sequence analy.

A;Reference number: S65801; MUID:97002551; PMID:8849898
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A;Residues: 1-273 <BED>
A;Cross-references: UNIPROT:P20826; UNIPARC:UPI0000028C9B; EMBL:U44725; NID:g1172215; Pi
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Mol. Biol. Cell 3, 349-352, 1992
A;Title: Differential expression and processing of two cell associated forms of the kit-A;Reference number: A43751; MUID:92330001; PMID:1378327
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A; Residues: 1-214, 'L', 216-273 <HUA>
A; Residues: 1-214, 'L', 216-273 <HUA>
A; Residues: 1-214, 'L', 216-273 <HUA>
A; Notes: the authors translated the codon TTG for residue 215 as Trp
R; Huang, E.; Nocka, K.; Beier, D.R.; Chu, T.Y.; Buck, J.; Lahm, H.W.; Wellner, D.; Ledex
Cell 63, 225-233, 1990
A; Title: The hematopoietic growth factor KL is encoded by the Sl locus and is the ligan
A; Reference number: A35976; MUID:91004221; PMID:1698557
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A;Cross-references: UNIPARC:UPI000017955D; GB:M38511
R;Anderson, D.M.; Lyman, S.D.; Baird, A.; Wignall, J.M.; Eisenman, J.; Rauch, C.; March, Cell 63, 235-243, 1990
A;Title: Molecular cloning of mast cell growth factor, a hematopoietin that is active in A;Reference number: A35977; MUID:91004223; PMID:1698558
                                     stem cell factor isc
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J. Biol. Chem. 266, 8102-8107, 1991
A; Title: Amino acid sequence and post-translational modification of A; Reference number: A39805; MUID:91217037; PMID:1708771
A; A; A; Cession: A39805
A; Status: preliminary
A; Rolecule type: protein
A; Residues: 'E', 27-190 eluNa>
A; Residues: 'E', 27-190 eluNa>
A; Cross-references: UNIPARC:UPI000014F57C
C; Superfamily: mouse mast cell growth factor
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                                                                                                                                                                                                                                                                                                            Query Match 80.8%; Score 857; DB 2; Length 20
Best Local Similarity 82.6%; Pred. No. 1.3e-60;
Matches 166; Conservative 15; Mismatches 20; Indels
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A;Molecule type: mRNA
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C;Species: Rattus norregicus (Norway rat)

C;Species: Rattus norregicus (Norway rat)

C;Species: Rattus norregicus (Norway rat)

C;Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 09-Jul-2004

C;Accession: B35974; A39805

R;Martin, F.H.; Suggs, S.V.; Langley, K.B.; Lu, H.S.; Ting, J.; Okino, K.H.; Morris, C.F.

B; J.C.; Patel, A.C.; Fisher, B.F.; Erjavec, H.O.; Herrera, C.J.; Wypych, J.; Sachdev, R.

A;Reference number: A35974; MUD:91004219; PMID:2208279

A;Reference number: A35974; MUD:91004219; PMID:2208279

A;Accession: B35974

A;Accession: B35974

A;Molecule type: mRNA

A;Residues: 1-201 cMAR>

A;Residues: 1-201 cMAR>

A;Cross-references: UNIPROT:P21581; UNIPARC:UPI0000144090; GB:M59966; NID:g206861; PIDN:

R;Lu, H.S.; Clogston, C.L.; Wypych, J.; Fausset, P.R.; Lauren, S.; Mendiaz, B.A.; Zsebo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gibecies: Canis lupus familiaris (dog)
CiSpecies: Canis lupus familiaris (dog)
CiSpecies: Canis lupus familiaris (dog)
CiSpecies: Odice cap-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
CiAccession: 146229
RiShull, R.M.; Suggs, S.V.; Langley, K.B.; Okino, K.H.; Jacobsen, F.W.; Martin, F.H.
Exp. Hematol. 20, 1118-1124, 1992
A;Title: Canine stem cell factor (c-kit ligand) supports the survival of hematopoietic particles canine stem cell factor (c-kit ligand) supports the survival of hematopoietic particles canine stem cell factor (c-kit ligand) supports the survival of hematopoietic particles preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: UNIPROT: Q06220; UNIPRAC: UPI000013563A; GB:S53329; NID: g262240; PIDN: C;Superfamily: mouse mast cell growth factor
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                                                                                                                                                            MDVLPSHCWISEMVVQLSDSLTDLLDKPSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                  KOLKKSFKSPBPRLFTPEEFFRIFNRSIDAFKDF-VVASETSDCVVSSTLSPEKDSRVSV 179
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Cell 64, 1025-1035, 1991
A,Title: Transmembrane form of the kit ligand growth factor is determined by alternative A,Title: Transmembrane form of the kit ligand growth factor is determined by alternative A,Reference number: A37934; MUID:91160046; PMID:1705866
A,Accession: A37934
A,Accession: A37934
A,Residues: 1-245 < FLA>
                                                                                                                                                                                              A.Cross-references: UNIPROT: P20826; UNIPARC: UPI000002B352; GB:M64262
R.Huang, E.J.; Nocka, K.H.; Buck, J.; Besmer, P.
Mol. Biol. Cell 3, 349-362, 1992
Myl. Biol. Cell 3, 349-362, 1992
A.Fitle: Differential expression and processing of two cell associated forms of the kit. A.Reference number: A43751; MUID:92330001; PMID:1378327
A.Accession: B43751
                                                                                                                                                                                                                                                                                                                                                                                                     A)Status: preliminary
A)Molecule type: mRNA
A)Residues: 1-173, R',175-186,'L',188-245 <HUA>
A)Cross-references: UNIPARC:UPI0000179560; GB:S04534
A)Note: the authors translated the codon TTG for residue 187 as Trp
C)Superfamily: mouse mast cell growth factor
                  Chan, D.C.; Leder,
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A;Residues 1-273 cAND>
A;Residues 1-273 cAND>
A;Residues 1-273 cAND>
A;Residues 1-273 cAND>
A;Cross-references UNIPARC;UPI0000028C9B; GB:NE7647, GB:N38436; NID:g199151; PIDN:AAA33 R;Copelland, NG.; GGIDEC, D.J.; Cho, B.C.; Donovan, P.J.; denkins, N.A.; Cosman, D.; An Call G, 175-183, 1990
A;Tile Nate cell growth factor maps near the steel locus on mouse chromosome 10 and is A;Recession: A5972
A;Reterence number: A3972; MUID:91004216; PMID:1598554
A;Reterence number: A3972; MUID:91004216; PMID:1598554
A;Reterence number: A3972; MUID:91004218; DR:N59912
A;Reterence number: A3975; MUID:91004220; PMID:1698556
A;Reterence number: A3975; MUID:91004220; PMID:1208278
A;Reterence number: A35975
A;Reterence number: A35975
A;Reterence number: A35975
A;Reterence number: A35975
A;Reterence number: A35973; MUID:91004218; PMID:208278
A;Reterence number: A35973; MUID:91004218; PMID:208278
A;Reterence number: A35973; MUID:91004218; PMID:208278
A;Reterence number: A35973; MUID:91004218; PMID:30877
A;Reterence number: A35973; MUID:91004218; PMID:30877
A;Reterence number: A35973; MUID:91004218; PMID:30877
A;Reterence number: A35973; MUID:9100401955F
B;Reternce number: A35973; MUID:91004018; PMID:30877
A;Reterence number: A4071; MUID:93012940; PMID:3995283; PIDN:CAMA8778.1; PM:A;Reternce number: A4071; MUID:93012940; PMID:3995283; PIDN:CAMA8778.1; PM:A;Reternce number: A4071; MUID:93012940; PMID:3995283; PIDN:CAMA8778.1; PM:A;Reternce number: A4071; MUID:93012940; PMID:3995283; PMID:3995283; PIDN:CAMA8778.1; PM:A;Reternce number: A4071; MUID:93012940; PMID:3995283; PMID:3995283; PMID:39954111; PM:A;Reternce number: A4071; MUID:93012940; PMID:3995283; PMID:3995283; PMID:39954111; PM:A;Reternce number: A4071; MUID:93012940; PMID:399595; NID:3995283; PMID:39954111; PM:A;Reternce number: A4071; PM:A;Reternce number: A40
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mast cell growth factor precursor (version 2) - mouse
N;Alternate names: KL-2 protein
C;Species: Mus musculus (house mouse)
C;Species: Aul-1991 #sequence_revision 26-Jul-1991 #text_change 09-Jul-2004
C;Accession: A37934; B43751
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Best Local Similarity 82.3%; Pred. No. 2.8e-60;
Matches 167; Conservative 16; Mismatches 20,
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stem cell factor - human (fragments)
c;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens
C;Accession: S29052
R;Lu, H.S.; Clogston, C.L.; Wypych, J.; Parker, V.P.; Lee, T.D.; Swiderek, K.; Baltera J.; Langley, K.S.
Langley, K.S.
Arch. Biochem. Biophys. 298, 150-158, 1992
A;Title: Post-translational processing of membrane-associated recombinant human stem cel
A;Reference number: S29052; MUID:92398336; PMID:1381905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Accession: S29052
A,Status: preliminary
A,Molecule type: protein
A,Residues: 1-13;14-30;31-46;47-59;60-86;87-95;96-107;108-124 <LUH>
A,Residues: UNIPROT: Q7M4N8; UNIPARC: UPI0000179563; UNIPARC: UPI0000179564; UNIPARC
C,Superfamily: mouse mast cell growth factor
                                                                 ö
                                                                                                                                                                                                                                            MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                        61 MDVLPSHCWLRDMVIQLSLSLTTLLDKFSNISEGLSNYSIIDKLGKIVDDLVLCMEENAP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSSKDLKKSFKSPEPRLFTPEEFFRIFN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                    1 MKKTQTWIITCIYLQLLLFNPLVKTKBICGNPVTDNVKDITKLVANLPNDYMITLNYVAG
                                                                                                                         1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPGMDVLPSHCWISEMVVQLSDSLTDLL
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                              KOLKKSPEKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Length 124;
Query Match 67.4%; Score 715; DB 2; Length 245; Best Local Similarity 79.8%; Pred. No. 2.8e-49; Matches 138; Conservative 16; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 RSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVTKPFMLPPVAA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 576.5; DB
Pred. No. 1e-38;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 54.3%;
Best Local Similarity 75.2%;
Matches 124; Conservative (
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mast cell growth factor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 09-Jul-2004
C;Accession: B33971
R;Williams, D.B.; Bisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park, J A;Title: Identification of a ligand for the c-kit proto-oncogene.
A;Title: Identification of a ligand for the c-kit proto-oncogene.
A;Reference number: A35971; MUID:91004215; PMID:1698553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Species: Coturnix coturnix (quail)
C:Species: Coturnix coturnix (quail)
C:Date: 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
C:Date: 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
C:Date: 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
R:Petites. 130367
B:Petites. 13036
A:Title: Cloning and characterization of cDNAs encoding two forms of avian stem cell facesion: 57036; MUD:96283808; PMID:8679698
A:Accession: 570367
A:Molecule type: mRNA
A:Molecule type: mRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 MDSLPNHCWILHLAVVPEPSRSLHNILQKFVDISDMSDVLSNYSIINNITRIINDLAARCLAF 120
118 NSSKD-LKKSFKSPEPRLFTPEBEPRIFNRSIDAFKUFVYKEFADSLDKNDCIMPSTVETPENDS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 NSSKD-LKKSFKSPEPFRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTL-SPEKDS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 MDVLPSHCWISEMVVQLSDSLTDLLDKF---SNISEGLSNYSIIDKLVNIVDDLVECVKG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKKAQTWIITCFCLQLLLINPLVKTQSSCGNPVTDDVNDIAKLVGNLPNDYLITLKYVPK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indele
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C; Superfamily: mouse mast cell growth factor
C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 16.5%; Score 175.5; DB 2; Best Local Similarity 72.3%; Pred. No. 1.6e-07; Matches 34; Conservative 5; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 45.2%; Score 479.5; DB 2; Best Local Similarity 46.9%; Pred. No. 1.2e-30; Matches 100; Conservative 42; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 RVSVTKPFMLPPVAASSLRNDSSSSNSKYIYLI 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  stem cell factor short form precursor - quail
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A;Molecule type: protein
A;Residues: 1-51 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Accession: B35971
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Surveys.

Surveys.

C; Species: Gallus gallus (chicken)

C; Species: Gallus gallus (chicken)

C; Species: Gallus gallus (chicken)

C; Dates 24-Peb-1994 #text_change 09-Jul-2004

C; Dates 124. 269-2190, 1993

R; Zhou, J.H.; Ohtaki, M.; Sakurai, M.

Gene 127, 269-270, 1993

A; Title: Sequence of a cDNA encoding chicken stem cell factor.

A; Reference number: JN0637; MUID: 93273244; PMID: 7684722

A; Reference number: JN0637

A; Molecule type: mRNA

A; Residues: 1-287 < ZHO>

A; Molecule type: mRNA

A; Residues: 1-287 < ZHO>

A; Cross references: UNTRROT: Q09108; UNIPARC: UPI000013563C; GB: D13516; NID: G391648; PIDN:

A; Cross references: UNIPARD: Are a cell growth factor

C; Superfamily: mouse mast cell growth factor

C; Superfamily: signal sequence #status predicted < SIG>
F; 26-281/Product: stem cell factor #status predicted < NMA>

F; 226-248/Domain: transmembrane #status predicted < TMM>
                                                                                                                                                                                                                                                                                                         fac
                                                                                            C.Species: Coturnix coturnix (quain)
C.Species: Coturnix coturnix (quain)
C.Date: 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
C.Date: 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
C.Date: 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
R.Petitte, J.N.; Kulik, M.J.
Biochim. Biophys. Acta 1307, 149-151, 1996
B.Petitte, J.N.; Kulik, M.J.
Biochim. Biophys. Acta 1307, 149-151, 1996
A.Refitte: Clouning and characterization of cDNAs encoding two forms of avian stem cell fan
A.Residues: 370366
A.Residues: 1-287 - PET->
A.Residues: 1-287 - PET->
A.Corss-references: UNIPARC:UPI000013563D; EMBL:U43078; NID:g1150875; PIDN:AAC59933.1; IC.Superfamily: mouse mast cell growth factor
C.Superfamily: mouse mast cell factor long form #status predicted <MAT>
F:1-25/Domain: signal sequence #status predicted <TWM>
F:226-287/Product: stem cell factor long form #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NSSKO-LKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTL-SPEKDS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MDVLPSHCWISEMVVQLSDSLTDLLDKFSNI----SEGLSNYSIIDKLVNIVDDLVECVKE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 53.8%; Score 570.5; DB 2; Length Best Local Similarity 55.1%; Pred. No. 8.8e-38; Matches 114; Conservative 37; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 53.0%; Score 562.5; DB 2; Length Best Local Similarity 54.6%; Pred. No. 3.8e-37; Matches 113; Conservative 36; Mismatches 53; Indels
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                                                                stem cell factor long form precursor - quail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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RESULT 15
A35971
mast call growth factor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 09-Jul-2004
C;Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change N. March, C.J.; Park, I.R.
A;Reference number: A35971; MuID:91004215; PMID:1698553
A;Retus: preliminary
A;Molecule type: protein
A;Residues: 1-49 *MIL.
A;Residues: 1-49 *MIL.
A;Residues: 1-49 *MIL.
A;Residues: 1-49 *MIL.
A;Coss-references: UNIPROT:P20826; UNIPARC:UP10000179561
C;Superfamily: mouse mast cell growth factor
C;Reywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 16.3%; Score 172.5; DB 2; Length 49; Best Local Similarity 73.5%; Pred. No. 2.6e-07; Matches 36; Conservative 4; Mismatches 6; Indels 3;
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Search completed: February 22, 2006, 18:20:26 Job time : 19.1901 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Pebruary 22, 2006, 18:05:51 ; Search time 107.152 Seconds
(without alignments)
1369.555 Million cell updates/sec Run on:

US-10-620-642-46 1061 1 MKKTQTWILTCIYLQLLLFN......AASSLRNDSSSSNSKYIYLI 208 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 seqs, 705528306 residues Searched:

2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		9 felis silve) sus scrofa					_	canis famil	1 rattus norv	8 mustela vis	mus	mus	_	9 macaca mula		4 rattus norv	3 homo sapien		gallus gall	4 mus musculu		ambystom	0 xenopus lae		3 xenopus lae		-			2 plasmodium
	Descr	P21583	P79169	029030	Q95md2	086524	P79368	028132	Q95m19	006220	P21581	095n18	064384	078ed8	P20826	086419	Q68dz2	Q54a14	Q7m4n8	090314	009108	261854	28c9k1	09ygp2	272xv0	28ayn7	Q6dtw3	0 56jh6	Q481a5	Q 56jh5	28 i fm	28тмр2
	d di	_			SCF_HORSE		SCP_SHEEP P			SCF_CANFA				Q78ED8_MOUSE Q							SCF_CHICK 0		OUSE	AMBME	ENLA	XENLA	KENLA		Q4S1A5_TETNG Q	BRARE	PLAF7	Q8MWP2_PLAFA Q
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	Match Length DB	273	274	274	274	245	267	274	274	274	273	274	208	208	273	164	238	245	124	287	287	123	160	271	270	270	270	272	234	267	1697	1711
% Query	Match	97.1	85.6	84.8	84.7	83.9	83.8	83.6	83.5	81.3	81.1	81.0	90.6	80.6	90.6	78.7	75.8	68.0	54.3	53.8	53.0	48.0	45.2	30.8	28.2	25.8	25.5	17.3	14.0	11.7	11.0	11.0
	Score	1030	908.5	899.5	898.5	890	889.5	886.5	885.5	862.5	861	859.5	855	855	855	835	804	721	576.5	570.5	562.5	509	480	327	299.5	273.5	270.5	184	149	124	116.5	116.5
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plasmodium plasmodium plasmodium	candida gla dictyosteli caenorhabdi ashbya goss	emericella emericella rickettsia vibrio para candida gla
Q8mwp1 Q8mwh2 Q6ya77		Q96746 Q9684 Q9633 Q8733 Q6748
Q8MWP1 PLAFA Q8MWH2 PLAFA Q6YA7 PLARE	092645 CIVV 06FLY9 CANGA 054UK3 DICDI 019545 CAREL 075FP AAHGO	Q96VKG_EMENI Q9P684_EMENI SCA4_RICPE Q87M34_VIBPA Q6FV48_CANGA
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116.5	99 97.5 97.5	96.5
266	, w w w w 4	. 4 4 4 4 5 4 5 6 7

ALIGNMENTS

RESULT 1 SCF_HUMA ID SCF	RESULT 1 SCF HUMAN ID SCF HUMAN STANDARD; PRT; 273 AA.
AC DT	P21583; Q16487; Q9UQK7; 01-MAY-1991 (Rel. 18. Created)
i di	01-MAY-1991 (Rel. 18, Last sequence update)
1 E	lu-Mar-2005 (Rel. 47, mast annocation update) Kit liqand precursor (C-kit liqand) (Stem cell factor) (SCF) (Mast
DE	cell growth factor) (MGF).
Z S	Name=KIILG; Synonyms=MGF, SCF; Homo saniens (Human).
8	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
88	Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae; н.т.
88	NCBI_TAXID=9606;
2 5	Wisterian contrava (10000b)
žž	NOCLEGILLE SECUENCE (ISOCOMP 1/. MEDLINE=91004219; Pubmed=2208279; DOI=10.1016/0092-8674(90)90301-T;
RA 6	Martin F.H., Suggs S.V., Langley K.E., Lu H.S., Ting J., Okino K.H.,
§ \$	MAITH K.A., Johnson M.J., Parker V.P., Flores J.C., Patel A.C.,
æ	Fisher E.F., Erjavec H.O., Herrera C.J., Wypych J., Sachdev R.K.,
R.	Pope J.A., Leslie I., Wen D., Lin CH., Cupples R.L., Zsebo K.M.;
R E	Princary structure and functional expression of rat and numan stem
7 E	Cell 1203-211(1990)
2	
ЯÞ	NUCLEOTIDE SEQUENCE (ISOFORM 2).
ž:	PubMed=1724381;
\$ 2	Anderson D.M., Williams D.E., Tushinski K., Gimpel S., Ebsenman U.,
5 £	Cannizario L.A., Alchibon m., ticce c.m., nucluel k., comman. J.; "Alternate splicing of mRNAs encoding human mast cell growth factor
RT	and localization of the gene to chromosome 12q22-q24.";
RL	Cell Growth Differ. 2:373-378(1991).
S. S.	(3) with sometime controller (Technolm 2)
2 2	MODINE=9166429; PubMed=10049787; DOI=10.1006/bbrc.1999.0260;
æ	Blair H.C., Julian B.A., Cao X., Jordan S.E., Dong S.S.;
R.	"Parathyroid hormone-regulated production of stem cell factor in human
7 Z	OsteoDiagne and OsteoDiagner Tito, Oct. 1999). Biochem Richham Recommin 255:778-784 (1999).
æ	(4)
RP	NUCLEOTIDE SEQUENCE.
5	Han C., Peng X., Yuan J., Qiang B.;
2 Z	Submitted (JUL-2001) to the KMBL/Genbank/DUBJ databases. [6]
2 2	ILL. INC. FOUTDE SEQUENCE [LARGE SCALE MENA] (ISOFORM 1).
2	WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
æ	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.
2 2	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
¥ 6	Altegolul S.K., Zeeberg B., buctow K.H., Schaefer L.E., but. Honking P. Fordan H. Moore T. Max S.T. Wang J. Heieh F.
5 2	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

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SCF_FELCA
P79169;
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TRANSMEM
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STE_FRECA
STE_FRECA
STE_FRECA
DT 28-FE
DT 28-FE
DT 10-MA
DB Kit 1
CC Felin

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Similarity).

Sutremarive splicing; Named isoforms=2;

Event-alternative splicing; Named isoforms=2;

Event-alternative splicing; Named isoforms=2;

Name=1; Synonyms=SCF248;

IsoId=P21583-1; Sequence=Usp 006022;

IsoId=P21583-2; Sequence=VSP 0060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                               Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J., Bosak S.A., McKenan P.J., McKernan K.J., Malek, Ganarathe P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y. Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Shonfard S.S.M., Krzywinski M.I., Skalska U., Smailus D.E., Sphnerch A., Schein J.B., Jones S.J.M., Marra M.A.,
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GO; GO:0005173; F:stem cell factor receptor binding; NAS.
GO; GO:0008283; P:cell proliferation; TAS.
GO; GO:000807; P:hemopoiesis; NAS.
GO; GO:007165; P:signal transduction; TAS.
InterPro; IPR012351; Cytokine_4_hix.
InterPro; IPR03452; SCF.
PANTHER; PTHR11574; SCF; 1.
                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences."; . Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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EMBL, AF119835; AAA022048 1; mRNA.
EMBL, AF400436; AAA02408.1; mRNA.
EMBL, AF400437; AAK02486.1; -; mRNA.
EMBL, BC069733; AAH69733.1; -; mRNA.
EMBL, BC069733; AAH69733.1; -; mRNA.
EMBL, BC069797; AAH69793.1; -; mRNA.
EMBL, S42571; ABA2246.2; -; mRNA.
EMBL, S42571; ABA2246.2; -; mRNA.
PIR, A35974; A35974.
PIR, BA1190; B61190.
PDB; 1ECF; X-ray; A/B/C/D=26-166.
PDB; 1ECF; X-ray; A/B/C/D=26-166.
PDB; 1ECF; X-ray; A/B/C/D=26-166.
PDB; 1SCF; X-ray; A/B/C/D=26-166.
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MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WUCLECTIDE SEQUENCE (ISOPORMS 1 AND 2).

MUCLECTIDE SEQUENCE (ISOPORMS 1 AND 2).

MEDLINE=97069946; PubMed=8912926;

Dunham S.P., Onions D.E.;

The cloning and sequencing of cDNAs encoding two isoforms of feline stem cell factor.";

DNA Seq. 6:233-237(1996).

-I- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).

-I- SUBGNIT: Homodimer, non-covalently linked (Probable).

-I- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).

Also exists as a secreted soluble form (isoform 1 only) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKKTQTWILICIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLFKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
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28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 41, Last annotation update)
11-MAY-2005 (Rel. 41, Last annotation update)
11-MAY-2005 (Rel. 41, Last annotation update)
12-MAMP-2007 (MGF).
13-MAMP-3007 (MGF).
14-MAMP-3009 (Cat).
15-MAMP-3009 (Cat).
15-MAMP-3009 (Cat).
15-MAMP-3009 (MGATA) (Carniata; Vertebrata; Buteleostomi; MAMP-3009 (MGATA).
15-MAMP-3009 (MGATA) (Carniata; Carnivora; Fissipedia; Felidae;
                                                                          Kit ligand.

Extracellular (Potential).

Potential.

Cycplasmic (Potential).

N-linked (GlcNAc. ..) (Potential).

By similarity.

By similarity.

By similarity.

By similarity.

By similarity.
3D-structure; Alternative splicing; Cell adhesion; Glycoprotein;
Growth factor; Signal; Transmembrane.
SIGNAL 1 25
                                                                                                                                                                                                                                                                                                                                                                                                                            55 55 L -> S (in Ref. 3 and 4; AAK92486)
128 128 K -> R (in Ref. 3 and 4; AAK92486)
134 134 L -> P (in Ref. 3 and 4; AAK92486)
273 AA; 30899 MW; 19FD362CB59C6607 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1030; DB 1; Length 273; Pred. No. 2.2e-71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.18;
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                                                             Local Similarity
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NCBI_TaxID=9685;
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215
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1; Gaps 1;
                                                                                                                            This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BNBL outstation — the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ENVKKSSKSPEPRLFTPEKFPGIFNRSIDAFKDLEMVAPKTSECVISSTLTPEKDSRVSV 180
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Growth factor; Signal; Transmembrane. By similarity.
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(Potential).
(Potential).
(Potential).
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Extracellular (Potential).
Cytoplasmic (Potential).
N-linked (GlCNAC. .) (Pot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF3C87114D7BA6A6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, L07786; AAA53670.1; -; mRNA.
PIR; 146575; 146575.
SMR; Q029030; 29-161.
InterPro; IPR012351; Cytokine 4 hlx.
InterPro; IPR012452; SCP.
PANTHER; PTHR11574; SCP; 1.
Pfam; PF02404; SCF; 1.
Cell adhesion; Glycoprotein; Growth fair SIGNAL.
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Matches 176; Conservative
                                                                                                [1]
NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                 This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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(29030).
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
Name=KTILG; Synonyms=MGF;
Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Potential.

Cytoplasmic (Potential).

N-linked (GlCNAc. .) (Potential).

N-linked (GlCNAc. .) (Potential).

N-linked (GlCNAc. .) (Potential).

By similarity.

By similarity.

By similarity.

By similarity.
                                                                                                                               "ISOId=P79169-2; Sequence=VSP 006021;
-!- PTM: A soluble form is produced by proteolytic processing of isoform 1 in the extracellular domain (By similarity).
-!- SIMILARITY: Belongs to the SCP family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 88.2%; Pred. No. 5.2e-62;
Matches 180; Conservative 13; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C5B78DB4791237BE CRC64;
                                           Event=Alternative splicing; Named isoforms=2;
Name=1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VSP_006021,
                                                                            IsoId=P79169-1; Sequence=Displayed;
Name=2;
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         BIMILATICY).
ALTERNATIVE PRODUCTS:
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Murray J.D., Bowling A.T.,
T. A primary Harry Hundle Comparative gene map.";
T. A primary Hundle Comparative gene map.";
Submitted (JAN-2000) to the BYBL/GenBank/DBB databases.
C.-I. FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).
C.-I. SUBGNIT: Homodimer, non-covalently linked (Probable).
C.-I. SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a secreted soluble form (By similarity).
C.-I. SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a secreted soluble form is produced by proteolytic processing of the extracellular domain (By similarity).
C.-I. SIMILARITY: Belongs to the SCF family.
                                SCF HORSE STANDARD; PRT; 274 AA.
095MD2; 062765; 095MG3; 095MG8; 09N1Y5;
28-FRB-2003 (Rel. 41, Created)
28-FRB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
Name=KITLG; Synonyms=MGF, SCF;
                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Skin;
Rieder S., Checa-Cortes M.L., Joerg H., Stranzinger G.;
Ran equine sequence homologous to stem cell factor (KIT-ligand).";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Terry R.R., Bailey E.F., Cothran E.G.; "Evaluation of MGF as the candidate gene for Appaloosa spotting."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kit ligand.
Extracellular (Potential).
Potential.
Cytoplasmic (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE OF 4-264.
Terry R.R., Mickelson J.R., Schmutz S., Cothran E.G., Bailey "Eguus caballus mast call growth factor (MGF)."; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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EMBL; AF053498; AAC97076.1; -; mRNA.
EMBL; AF367704; AAK63249.1; -; Genomic_DNA.
EMBL; AF367706; AAK63250.1; -; Genomic_DNA.
EMBL; AF130770; AAF36716.1; -; Genomic_DNA.
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InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR003452; SCF.
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PANTHER; PTHR11574; SCF; 1.
Pfam; PPC43404; SCF; 1.
Cell adhesion; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9796;
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Bukaryotyn Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;

Cercopithecidae; Cercopithecinae; Papio.
                                                                                                                                                                                                                       7;
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                                                                                                                                                                       DB 1; Length 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.9%; Score 890; DB 2; Length 245; 100.0%; Pred. No. 1.2e-60; rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WUCLECTIDE SEQUENCE.
Stalina T., Storek J.;
Stalina T., Storek J.;
Stalina T., Storek J.;
EMBL, AX226584; AA072537.1; -; mRNA.
EMBL, AX226584; AA072537.1; -; mRNA.
EMBL, AX226584; AA072537.1; -; mRNA.
SWR; Q86524; 29-161.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005173; F:serem cell factor receptor binding; IEA.
GO; GO:0007155; F:cell adhesion; IEA.
                                                                                                                                                                                                                    11; Indels
N-linked (GlcNAc. . .) (Pot
By similarity.
By similarity.
Q -> P (in Ref. 2).
Missing (in Ref. 3).
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SEQUENCE 245 AA; 27887 MW; 937B3CAF28D694FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0865247
01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-UNR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                  Query Match

84.7%; Score 898.5; DB 1
Best Local Similarity 86.8%; Pred. No. 3.1e-61;
Matches 177; Conservative 15; Mismatches 11
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  207 207 N-:
29 114 By
68 164 By
15 15 0 .
241 241 Mi.
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15; Mismatches 13; Indels

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Matches 175; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOKINE 11:249-256 (1999).

-!- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a secreted soluble form (By similarity).
-!- PTM: A soluble form (By similarity).
-!- PTM: A soluble form (By similarity).
                                   PV9368; Q28591; 28-PEB-2003 (Rel. 41, Created) 28-PEB-2003 (Rel. 41, Latt sequence update) 28-PEB-2003 (Rel. 41, Latt sequence update) 10-MAY-2005 (Rel. 47, Latt annuation update) Kit ligand precursor (C-kit ligand) (Stem cell factor) (MGP) (Pragment). Name=KITLG; Synonyms=SCF; Name=KITLG; Synonyms=SCF; Ovis arise "------ "hordata: Craniata: Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tisdall D.J., Quirke L.D., Galloway S.M.;
"Ovine stem cell factor gene is located within a syntenic group on chromosome 3 conserved across mammalian species.";
Mamm. Genome 7:472-473 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99263397; PubMed=10328863; DOI=10.1006/cyto.1998.0430; MCInnes C.J., Deane D., Thomson J., Broad A., Haig D.M.; MThe cloning and expression of the colon for stem cell factor (kit-ligand) and characterization of its in vitro haematopoietic
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(ytoplamic (Potential).

N-linked (GlCNAc. .) (Potential).

N-linked (GlCNAc. .) (Potential).

N-linked (GlCNAc. .) (Potential).

N-linked (GlCNAc. .) (Potential).

By similarity.

By similarity.
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Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUR=Ovarian follicle;
MEDLINE=96413880; PubMed=8662240; DOI=10.1007/8003359900142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kit ligand.
Extracellular (Potential).
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                       267 AA.
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InterPro; IPR03452; SCF.
PANTHER; PTHR11574; SCF; 1.
Pfam; PF02404; SCF; 1.
Cell adhesion; Glycoprotein; Growth
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EMBL; Z50743; CAA90620.1; -; mRNA.
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SMR; P79368; 29-161.
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196
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Length 267;

Score 889.5; DB 1; Pred. No. 1.5e-60;

83.8%; 85.8%;

Best Local Similarity

Query Match

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OCE 132; OSTUT4;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
11-Mayar-2005 (Rel. 41, Last annotation update)
11-Mast (Schonyms-SCF)
Name=KITLG; Synonyms-SCF;
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                                                                               MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                       61 MDVLPSHCWISENVEQLSVSLTDLLDKFSNISEGLSNYSIIDKLVKIVDDLVECMEEHSF 120
                                                                                                                                                                   KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDF-VVASETSDCVVSSTLSPEKDSRVSV 179
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X MEDLINE=99315311, PubMed=10384045; DOI=10.1007/e003359901076;

Seitz J.J., Schmutz S.M., Thue T.D., Buchanan F.C.;

Seitz J.J., Schmutz S.M., Thue T.D., Buchanan F.C.;

The missense mutation in the bovine MGF gene is associated with the roan phenotype in Belgian Blue and Shorthorn cattle.";

Mamm. Genome 10:710-712(1999).

-I- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).

-I- SUBGELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2): Also exists as a secreted soluble form (isoform 1 only) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          οĘ
               MKKTQTW1LTC1YLQLLLPNPLVKTEG1CRNRVTNNVKDVTKLVANLPKDYM1TLKYVPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=2;
Isod=028132-2; Sequence=VSP 006020;
Isod=020able form is produced by proteolytic processing of
isoform 1 in the extracellular domain (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Bovine counterpart of stem cell factor.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE OF 204-239, AND VARIANT ASP-218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                        274 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bovine ētem cell factor.";
Biochim. Biophys. Acta 1223:148-150(1994).
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NCBI_TaxID=9913;
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SCF_CANFA
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                                                                        This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 MDVLPSHCWISEMVEQLSVSLTDLLDKFSNISEGLSNYCIIDKLVKIVDDLVBCWEEHSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKOF-VVASETSDCVVSSTLSPEKDSRVSV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLYMORPHISM: The roan locus is responsible for the coat coloration of Belgian Blue and Shorthorn cattle. The solid-colored and white animals are homozygotes, and the roan animals, with intermingled colored and white hairs, are heterozygous. The roan phenotype is due to the Asp-218 mutation. SIMILARITY: Belongs to the SCF family.
                                                                                                                                                                                                                                                                   Kit ligand.
Extracellular (Potential).
Extracellular (Potential).
Cytoplasmic (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
By similarity.
By similarity.
DSRYSVTKPFMLPPVAASSLRNDSSSSNR -> G (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Masi growth factor) (WGF).

cell growth factor) (WGF).
Capta hircus (Goat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                      Alternative splicing; Cell adhesion; Glycoprotein; Growth factor; Polymorphism; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                         13; Indels
                                                                                                                                                                                                                                                                                                                                                                                        /FTId=VSP 006020.
A -> D (in roan allele).
D6C1DDB77B0CB12B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                    83.6%; Score 886.5; DB 1
85.3%; Pred. No. 2.6e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274 AA
                                                                                                                                                     AB033716; BAA94808.1; -; mRNA. AF120154; AAD55355.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                  soform 2).
                                                                                                                                                                                                                                                             Potential.
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                                                                                                                                                                        PIR; S47571; S47571.
SMR; Q28132; 29-161.
InterPro; IPR012351; Cytokine 4 hlx.
InterPro; IPR013452; SCF.
PANTHER; PTHR11574; SCF; 1.
Pfam; PF02404; SCF; 1.
                                                                                                                                           EMBL; D28934; BAA06061.1; -; mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 85.34
Matches 174; Conservative
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274
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274 AA;
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216
239
239
239
90
1145
129
68
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                                                                                                                                                                                                                                                     Polymorphism;
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Q95M19;
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SEQUENCE
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Extracellular (Potential).

Potential.

Cytoplasmic (Potential).

N-linked (GlCNAc. .) (Potential).

N-linked (GlCNAc. .) (Potential).

N-linked (GlCNAc. .) (Potential).

N-linked (GlCNAc. .) (Potential).

By similarity.

By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Growth factor; Signal; Transmembrane
Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.5%; Score 885.5; DB 1; Length 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BBFE669A509EF65D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB002152; BAB71753.1; -; mRNA.
SMR; Q95M19; 29-161.
InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR003452; SCF.
                 Pecora; Bovidae; Caprinae; Capra.
NCBI_TaxID=9925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31053 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PANTHER, PTHR11574; SCF, 1.
Pfam, PF02404; SCF, 1.
Cell adhesion; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.3%;
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238
274
                                                                    NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEVELOPMENTAL STAGES. Acts in the early stages of hematopolesis. PTM: A soluble form is produced by proteolytic processing of the extracellular domain (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                        Schmutz S.M., Berryere T.G.;
"MGF sequencing in the dog aids in mapping to CFAIS.";
"MGF sequencing in the dog aids in mapping to CFAIS.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoletic progenitors in bone marrow culture. Mediates also cell-cell adhesion: Acts synergistically with other cytokines,
           Q06220; Q8SPM6;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
Name=KKTLG; Synonyms=MGF;
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probably interleukins.
SUBUNIT: Homodimer, non-covalently linked (Probable).
SUBCELLULAR LOCATION: Type I membrane protein. Also exists as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Growth factor; Signal; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Potential). (Potential).
                                                                                                                                                                                                                                                            Shull R.M., Suggs S.V., Langley K.E., Okino K.H., Jacobsen F.W.,
                                                                                                                                                                                                                                                                                            "Canine stem cell factor (c-kit ligand) supports the survival of hematopoietic progenitors in long-term canine marrow culture."; Exp. Hematol. 20:1118-1124(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Potential)
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Kit ligand.

Extracellular (Potential).

Potential.

Cytoplasmic (Potential).

Nlinked (GlCNAc. .) (Potential).

Nlinked (GlCNAc. .) (Potential).

Nlinked (GlCNAc. .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.3%; Score 862.5; DB 1; Length 84.8%; Pred. No. 1.8e-58; ive 13; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4182BE9AED00793B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; S53329; AAB24619.1; -; mRNA.

EMBL; AX094361; AAM16280.1; -; mRNA.

PIR; 146929; 146829.

SMR; Q06220; 29-161.

InterPro; IPRO12351; Cytokine_4_hlx.

InterPro; IPR003452; SCF.
 274 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Belongs to the SCF family.
 PRT;
                                                                                                                                                                                                                                                MEDLINE=93106145; PubMed=1281786;
                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE OF 17-274.
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Pfam; PF02404; SCF; 1.
Cell adhesion; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    secreted soluble form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 84.89
Matches 173; Conservative
STANDARD;
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215
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274
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196
196
29
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68
1
                                                                                                                                                                                NCBI_TaxID=9615;
                                                                                                                                                                                                                                  TISSUE=T-cell
                                                                                                                                                                                                                                                                               Martin F.H.;
                                                                                                                                                                                                                                                                                                                                                                           rissum=Tail:
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Gaps

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61 MDVLPSHCWISVWVBQLSVSLTDLLDKPSNISBGLSNYSIIDKLVKIVDDLVECTEGYSF 120
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MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
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PROTEIN SEQUENCE OF 26-190, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLECTIDE SEQUENCE OF 1-201, AND PARTIAL PROTEIN SEQUENCE.

NUCLECTIDE SEQUENCE OF 1-201, AND PARTIAL PROTEIN SEQUENCE.

MEDLINE-91004219; PubMed-2208279; DOI=10.1016/0092-8674(90)90301-T;

MARTIN F.H., Sugges S.V., Langley K.B., Lu H.S., Ting J., Okino K.H.,

Morris C.F., McNiece I.K., Jacobsen F.W., Mendiaz E.A., Birkett N.C.,

Smith K.A., Johnson M.J., Parker V.P., Plores J.C., Patel A.C.,

Fisher B.P., Erjavec H.O., Herrera C.J., Wypych J., Sachdev R.K.,

Pope J.A., Leslie I., Wen D., Lin C.-H., Cupples R.L., Zsebo K.M.;

Primary structure and functional expression of rat and human stem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN SEQUENCE OF 26-39.
MEDLINE-91004218; PubMed=2208278; DOI=10.1016/0092-8674 (90) 90300-4;
ZSEBD K.M., WYDYCH J., MCN1ece I.K., Lu H.S., Smith K.A.,
ZSEBD K.B., Sachdev R.K., Yuschenkoff V.N., Birkett N.C.,
Williams L.R., Satyagal V.N., Tung W., Bosselman R.A., Mendiaz E.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Buffalo; TISSUE=Liver;
MEDLINE=91217037; PubMed=1708771;
Lu H.S., Clogston C.L., Wypych J., Fausset P.R., Lauren S.,
Mendiaz E.A., Zebo K.M., Langley K.E.;
Mendiaz E.A., Zebo K.M., Langley K.E.;
"Amino acid sequence and post translational modification of stem cfactor isolated from buffalo rat liver cell-conditioned medium.";
J. Biol. Chem. 266:8102-8107(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Identification, purification, and biological characterization of hematopoietic stem cell factor from buffalo rat liver-conditioned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MXY-1991 (Rel. 18, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF)
cell growth factor) (MGF) (Hematopoietic growth factor KL).
Name=Kitlg; Synonyms=Mgf;
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Teramoto T., Nagashima M., Thorgeirsson S.S.; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P21581; Q9QWZ4; Q9Z2E7;
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181 KPFMLPPVAASSLRNDSSSSNRK 203

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NCBI_TaxID=9667;
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171
268
                                                          Q95N18; Q95MNS;
                                                                                                                                                                                                                                                                                                                                                        Name=2;
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                                                    This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 MDVLPSHCWLRDMVTHLSVSLTTLLDKFSNISEGLSNYSIIDKLGKIVDDLVACMEENAP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKKTQTWIITCIYLQLLLEPNPLVKTQBICRNPVTDNVKDITKLVANLPNDYMITLNYVAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
probably interleukins.
SUBUNT: Bumodimer, non-covalently linked (Probable).
SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).
Also exists as a secreted soluble form (isoform 1 only) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -> G (in
                                                                                                  ISOIG-P21581-2; Sequence-VSP 006025; DEVELOPMENTAL STAGE: Acts in the early stages of hematopoiesis. DEVELOPMENTAL STAGE: Acts in the early stages of hematopoiesis. PTM: A soluble form is produced by proteolytic processing of isoform 1 in the extracellular domain. SIMILARITY: Belongs to the SCF family.
                                                                                                                                                                                                                           EMBL; AF071204; AAD02827.1; -; mRNA.
EMBL; AF071205; AAD02828.1; -; mRNA.
EMBL; MS9966; AAA42117.1; -; mRNA.
EMBL; MS9966; AAA42117.1; -; mRNA.
ENR1; MS9966; AAA42117.1; -; mRNA.
ENR1; MS19974; BS3974.
SMR; P21581; 29-159.
ENRSHMG0000000005386; Rattus norvegicus.
InterPro; IPR012351; Cytokine_4-hlx.
InterPro; IPR012351; Cytokine_4-hlx.
InterPro; IPR01351; CSF; 1.
PANTHER; PTHR11574; SCF; 1.
Alternative splicing; Cell adhesion; Direct protein sequencing; Glycoprotein; Growth factor; Pyrrolidone carboxylic acid; Signal;
                                                                                                                                                                                                                                                                                                                                                                                              Potential.
Cytoplasmic (Potential).
Pyrrolidome carboxylic acid.
N-linked (GlcNAc. .); partial.
N-linked (Probable).
O-linked (Probable).
O-linked (Probable).
N-linked (Probable).
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Extracellular (Potential)
                                             similaticy.
similaticy:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15; Mismatches
                                                                       Name=1; Synonyms=KL-1;
IsoId=P21581-1; Sequence=Displayed;
Name=2; Synonyms=KL-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KPFMLPPVAASSLRNDSSSSNSK 203
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Matches 167; Conservative
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237
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273 AA;
                                          Bimilarity)
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                                                                                                                                                                                                                     Mustela vison (American mink).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Mustelidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        isoform 2).
/FIId=VSP_006024.
5 -> P (in Ref. 1; AAK73366).
5 -> N (in Ref. 1; AAK73366).
EREPOBY -> RESFEKRUNGFYHTVLSYLGG (in Ref. 1; AAK73366).
                                                                                                                                                                                                                                                                                                                                                                                                        Bennett R.D., Murphy B.D.;

Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).

-!- SUBCURIT. Homodimer, non-covalently linked (Probable).

-!- SUBCELLUIAR LOCATION: Type I membrane protein. Also exists as a secreted soluble form (By similarity).
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                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (Crit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
Name-KITLG; Synonyms-SCF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            adhesion; Glycoprotein; Growth factor;
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By similarity.
DSRVSVTKPFMLPPVAASSLRNDSSSSNR
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Extracellular (Potential).
Potential.
Cycoplasmic (Potential).
N-linked (GlCNAC. .) (Pot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=2;
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274 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=Q95N18-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMR; Q95N18; 29-161.
InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR003452; SCF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AY013712; AAG37434.1; -; mRNA.
EMBL; AF323757; AAK73366.1; -; mRNA.
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  STANDARD;
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Alternative splicing, C Signal; Transmembrane.
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MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WEDLINE=91160046; PubMed=1705866; DOI=10.1016/0092-8674(91)90326-T; Planagan J.G., Chan D.C., Leder P.; Planagan J.G., Chan J.G., Cha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKKTQTWILICIYLQLLLFNPLVKTBGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
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P20826; P97332; Q62524; Q64222; Q921N5;
01-FBB-1991 (Rel. 17, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCP) (Mast cell growth factor) (MGF) (Hematopoietic growth factor KL) (Steel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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82.3%; Pred. No. 5e-58;
ive 16; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23222 MW; C74DD639566EB817 CRC64;
                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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       181 KPFMLPPVAASSLRNDSSSSNRK 203
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                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, Kit ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003452; SCF.
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Matches 167; Conservative
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Q78ED8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
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SEQUENCE 208 AA;
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                              Name=Kitl;
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                                                                                                                                                                                                                                                                                                                                                                    MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDF-VVASETSDCVVSSTLSPEKDSRVSV 179
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                            Length 274;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        064384;
064384;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-2004 (TrEMBLrel. 26, Last annotation update)
C-kit ligand C-terminally truncated secreted form KL-Sld.
                                                                                                                                                 Indels
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GO; GO:005173; F:stem cell factor receptor binding; IEA
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IRR003452; SCF.
31035 MW; 5AC1619014AE5E72 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02404; SCF; 1.
SEQUENCE 208 AA; 23222 MW; C74DD639566EBB17 CRC64;
                                                                 Query Match 81.0%; Score 859.5; DB 1; Best Local Similarity 83.3%; Pred. No. 3.1e-58; Matches 170; Conservative 16; Mismatches 17;
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274 AA;
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SEQUENCE
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Cell 63
    NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
STRAIN-C57BL/6J; TISSUB-Cerebellum;
STRAIN-C57BL/6J; TISSUB-Cerebellum;
MEDLINB-22354683; DubMed=12466851; DOI=10.1038/nature01266;
Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
Nagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
Dalla B., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDILINE=97032534; PubMed=8875893; DOI=10.1007/s003359900247;
MEDILINE=97032534; PubMed=8875893; DOI=10.1007/s003359900247;
Graw J., Locester J., Neuhaeuser-Klaus A., Pretsch W., Schmitt-John T.;
"Molecular analysis of two new Steel mutations in mice shows a
transversion or an insertion.";
Mamm. Genome 7:843-846(1996).
                                                                                                                                 "Molecular cloning of mast cell growth factor, a hematopoietin that is active in both membrane bound and soluble forms.";
                                                                                                                                                                                                                                                                                                                                                                                                         NUCLECTIDE SEQUENCE (ISOFORM 1).
MEDLINE=93012940; PubMed=1383087;
Brannan C.I., Bedell M.A., Resnick J.L., Eppig J.J., Handel M.A.,
williams D.E., Lyman S.D., Donovan P.J., Jenkins N.A., Copeland N.G.;
"Developmental abnormalities in Steell7H mice result from a splicing
defect in the steel factor cytoplasmic tail.";
                                                                                                                                                                                                   MEDIAINE=92330001; PubMed=1378327;
Huang E.J., Nocka K.H., Buck J., Besmer P.;
"Differential expression and processing of two cell associated forms of the kit-ligand: KL-1 and KL-2.";
Mol. Biol. Cell 3:349-362(1992).
                                                                                                                                                                                                                                                                                                                   MEDLINE=91160046; PubMed=1705866; DOI=10.1016/0092-8674(91)90326-T; Flanagan J.G., Chan D.C., Leder P.; Transmembrane form of the kit ligand growth factor is determined by alternative splicing and is missing in the Sld mutant."; cell 64:1025-1035(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98025115; PubMed=9360640; DOI=10.1016/S1383-5726(97)00005-8; Graw J., Neuhauser-Klaus A., Pretsch W.; "Detection of a point mutation (A to G) in exon 5 of the murine Mgf gene defines a novel allele at the Steel locus with a weak
                                                          STRAIN=WCB6F1;
WEDLINE-91004223; PubMed=1698558; DOI=10.1016/0092-8674(90)90304-W;
Anderson D.M., Lyman S.D., Baird A., Wignall J.M., Eisenman J.,
Rauch C., March C.J., Boswell H.S., Gimpel S.D., Cosman D.,
Williams D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE (ISOFORM 1), AND VARIANTS SER-122; PRO-193 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE (ISOFORM 1), AND VARIANTS PRO-193 AND SER-207 STRAIN=C3H/E1; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bedell M.A., Copeland N.G., Jenkins N.A.; "Multiple pathways for Steel regulation suggested by genomic and sequence analysis of the murine Steel gene."; Genetics 142:927-934(1996).
                                                                                                                                                                                           NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2)
                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J;
MEDLINE=97002551; PubMed=8849898;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE (ISOFORM 1).
                                             NUCLEOTIDE SEQUENCE (ISOFORM 1).
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phenotype.";
Mutat. Res. 382:75-78(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=102/E1 x C3H/E1;
                                                                                                                                                             Cell 63:235-243(1990).
                                                                                                                                                                                                                                                                                                             STRAIN=WCB6F1;
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Remains S., Continue D.S., Hillochem N., Jackson J.J., Jarvie B.D., Romains A. Kawaji H., Kuwanawa Y., Kadisierki R.M., King B.L., Magnotto D.S., Walteis B., Marchikuni L., WcKenzie L., Whith H. S. Magnashima T., Manzek M. J., Lee Y., Lee Y., Leehard B., Machika L., Whith H. S. Magnashima T., Manzek M. J., Marchicumi L., McKenzie L., Mikhi H. S. Magnashima T., Manze M. J. Galdon T., Radio D., Ranachandran S., Barwasi T., Read J.C., King J. S., Ranachandran S., Marchensida T., Read J.C., Rang Y., Manzek K., Manzek M. J. Marchika J. S., Kingada K., Marking D. Sansballan T., Robensida T., Seeping C. J. Segolo M., Mang L. Manzek K., Manzek M., Mang J. J., Mangarak L., Walharded C., Kang Y., Wang J. Yang I. Yang I. Yang I. Yang I. J. Manzek M., Mang J. J., Manzek M., Manzek M., Mang J. J., Manzek M., Manz

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Search completed: February 22, 2006, 18:19:20 Job time : 110.152 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity).
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                 SOTING SET TWO SOCIOLO SET TWO SET TWO SET TWO SET TWO SET TWO SOCIOLO SET TWO SET TWO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                                                                                                                                                                    -1- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins.
--- SUBUNIT: Homodimer, non-covalently linked (Probable).
--- SUBCELULIAR LOCATION: Type I membrane protein (1soforms 1 and 2).
Also exists as a secreted soluble form (isoform 1 only) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing, Named isoforms=2;
Name=1; Synonyms=KL-1;
Isold=P20826-1; Sequence=Displayed;
Name=2; Synonyms=KL-2;
Isold=P20826-2; Sequence=VSP 006023;
-!- DEVELOPMENTAL STAGE: Acts in the early stages of hematopoiesis.
-!- PTM: A soluble form is produced by proteolytic processing of isoform 1 in the extracellular domain.
-!- SIMILARITY: Belongs to the SCF family.
PARTIAL PROTEIN SEQUENCE OF 26-78.
MEDLINE=91004215; Pubmed=1698553; DOI=10.1016/0092-8674(90)90297-R; Williams D.E., Eisenman J., Baird A., Rauch C., van Ness K., March C.J., Park L.S., Martin U., Mochizuki D.Y., Boswell H.S., "Identification of a ligand for the c-kit proto-oncogene."; Cell 63:167-174(1990).
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0846L9;
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
50F (Pragment).
MACCAG mulatta (Rhesus macaque).
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EMBL; M57647; AAA39538 1; -; mRNA.
EMBL; S69634; ABA22555.2; -; mRNA.
EMBL; X68989; CAA48778.1; -; mRNA.
EMBL; U44724; -; NOT ANNOTATED CDS; Genomic_DNA.
EMBL; U44725; AAC52447.1; -; mRNA.
EMBL; X95381; CAA44667.1; -; mRNA.
EMBL; X99322; CAA64667.1; -; mRNA.
EMBL; X99322; CAA676598.1; -; mRNA.
EMBL; X10287; CAA71329.1; -; mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity).
ALTERNATIVE PRODUCTS:
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86 DKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSSKDLKKSPKSPEPRLFTPEEFFRIFN 145
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Cercopithecidae, Cercopithecinae, Macaca.
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SMR; QG84619; 4-136.
GO; GO:001620; C:membrane; IEA.
GO; GO:0005173; F:stem cell factor recej
GO; GO:0007155; P:etl adhesion; IEA.
InterPro; IPRO03452; SCF.
Pfam; PPO2404; SCF; 1.
Cell adhesion; Transmembrane.
NON TER 1
NON TER 164
SEQUENCE 164 AA; 18430 MW; 6AFE3A568
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NUCLEOTIDE SEQUENCE.
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Mis Poso Blom (USOFO)

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US-08-836-252A-6
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                                                                                                                                                                                                 February 22, 2006, 18:19:42; Search time 25.2121 Seconds (without alignments) 682.074 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                       1061
1 MKKTQTWILTCIYLQLLLFN......AASSLRNDSSSSNSKYIYLI 208
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Issued Patents AA:*

(cgn2_6/ptodata/1/iaa/5_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6_COMB.pep:*

(cgn2_6/ptodata/1/iaa/H_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-09-224-683-46
US-09-224-683-46
US-09-224-683-46
US-09-624-325A-46
US-08-422-918-48
US-08-428-918-48
US-08-482-918-48
US-08-482-918-61
US-09-224-681-49
US-09-224-681-61
US-08-336-728A-48
US-08-336-728A-48
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US-09-635-251-49
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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No.
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28 1030 97.1 290 2 US-09-949-016-9393 Sequence 9393, Ap 2 1030 97.1 290 2 US-09-949-016-9394 Sequence 9394, Ap 30 1026 96.7 273 2 US-08-482-918-50 Sequence 50, Appl 31 1026 96.7 273 2 US-08-224-681-50 Sequence 50, Appl 32 1026 96.7 273 2 US-09-635-251-50 Sequence 50, Appl 34 1026 96.7 273 2 US-09-635-251-50 Sequence 50, Appl 34 1026 96.7 273 2 US-09-634-50 Sequence 50, Appl 35 1026 96.7 273 2 US-09-604-325A-50 Sequence 50, Appl 36 1001 94.3 126 2 US-09-604-325A-50 Sequence 50, Appl 37 975 91.9 424 4 PCT-US95-0386-14 Sequence 50, Appl 40 920 86.7 266 2 US-08-24-681-57 Sequence 57, Appl 41 920 86.7 266 2 US-09-224-681-57 Sequence 57, Appl 42 920 86.7 266 2 US-09-224-681-57 Sequence 57, Appl 43 920 86.7 266 2 US-09-224-681-57 Sequence 57, Appl 44 920 86.7 266 2 US-09-224-683-57 Sequence 57, Appl 45 920 86.7 266 2 US-09-224-683-57 Sequence 57, Appl 46 920 86.7 266 2 US-09-224-683-57 Sequence 57, Appl 47 920 86.7 266 2 US-09-224-683-57 Sequence 57, Appl 48 920 86.7 266 2 US-09-224-683-57 Sequence 57, Appl 48 920 86.7 266 2 US-09-224-683-57 Sequence 57, Appl 48 920 86.7 266 2 US-09-224-683-57 Sequence 57, Appl 48 920 86.7 266 2 US-09-224-683-57 Sequence 57, Appl 48 920 86.7 266 2 US-09-224-683-57 Sequence 57, Appl 48 920 86.7 266 2 US-09-224-683-57 Sequence 57, Appl 48 920 86.7 266 2 US-09-224-683-57 Sequence 57, Appl 48 920 86.7 266 2 US-09-224-683-57 Sequence 57, Appl 49 920 86.7 266 2 US-09-224-683-57 Sequence 57, Appl 49 920 86.7 266 2 US-09-224-683-57 Sequence 57, Appl 49 920 86.7 266 2 US-09-224-683-57 Sequence 57, Appl 49 920 86.7 266 2 US-09-224-683-57 Sequence 57, Appl 40 920 86.7 266 2 US-09-224-683-57 Sequence 57, Appl 40 920 86.7 266 2 US-09-224-683-57 Sequence 57, Appl 40 920 86.7 266 2 US-09-224-683-57 Sequence 57, Appl 40 920 86.7 266 2 US-09-224-683-57 Sequence 57, Appl 40 920 86.7 266 2 US-09-224-683-57 Sequence 57, Appl 40 920 86.7 266 2 US-09-224-683-57 Sequence 67, Appl 40 920 86.7 266 2 US-09-224-683-57 Sequence 67, Appl 40 920 86.7 266 2 US-09-224-683-57 Sequence 67, Appl 40 920 86.7 266 2 US-09
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Sequence 6, Application US/08836252A Sequence 6, Application: Sharkey, Andrew M. APPLICANT: Sharkey, Andrew M. APPLICANT: Sharkey, Andrew M. APPLICANT: Dellow, Kimberley A. TITLE OF INVENTION: HUMAN SCF, A SPLICE VARIANT THEREOF, ITS TITLE OF INVENTION: HUMAN SCF, A SPLICE VARIANT THEREOF, ITS TITLE OF INVENTION: HUMAN SCF, A SPLICE VARIANT THEREOF, ITS TITLE OF INVENTION: HUMAN SCF, A SPLICE VARIANT THEREOF, ITS TITLE OF INVENTION KESSLER, GOLDSTEIN & FOX, P.L.L.C. STREET: 1100 NEW YORK AVENUE, N.W. SUITE 600 CITY: WASHINGTON STATE: D.C. COUNTRY: USA ZIP: 2006 CITY: MASHINGTON STATE: PRODUMLY READABLE FORM: MEDIUM TYPE: Ploppy disk

COUNTRY: USA

ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,252A
FILING DATE: 31-JULY-1997
CLASSIFICATION 5346
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB95/02547
FILING DATE: 31-OCT-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: GB 9422293.2
FILING DATE: 04-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9508618.7
FILING DATE: 28-APR-1995
ATTORNEY/AGENT INFORMATION:
MAME: ROBERT W. ESWOND
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0623.0550000
TELECHOMINICATION INPERMATION:
TELECHOME: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LEMETHAL TYPE: DIOLEITYEE: PLOCETIN

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PAPLICANT: Zsebo, Krisztina M.
APPLICANT: Beselman, Robert A.
APPLICANT: Buselman, Rethod for Enhancing the Efficiency of Gene
TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
NUMBER OF SEQUENCES: 100
TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
NUMBER OF SEQUENCES: 100
CORRESPONDENCES ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: 111inois
COUNTRY: United States of America
ZIP: 60606-6402
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER RADABLE FORM
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPPERATING SYSTEM: PC-1005/MS-DOS
OPPERATING SYSTEM: PC-1005/MS-DOS
OPPERATING SYSTEM: PC-1005/MS-DOS
                     MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                    KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
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APPLICATION NUMBER: US/09/224,681
FILING DATE:
FILING DATE:
CLASSIFICATION:
PROR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 24-MAY-1998
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-MAY-1995
FILING DATE: 24-MAY-1990
FILING DATE: 15-MAY-1990
FILING DATE: 10-CT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/53,616
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION NUMBER: 07/537,198
FILING DATE: 16-OCT-1989
ATTONEY/AGENT INPOWMETTON:
ANAMER: 16-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEBRIONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                181 KPFMLPPVAASSLRNDSSSSNSKYIYLI 208
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Sequence 46, Application US/09224681
Patent No. 6207454
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Sequence 46, Application US/08482918

Patent No. 6207417

GENERAL INFORMATION:

APPLICANT: Zeebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Bosselman, Robert A.
APPLICANT: Bosselman, Francis H.
TITLE OF INVEXTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
COUNTRY: United States of America
ZITS: 6066-6402
COUNTRY: United States of America
ZITS: 6066-6402
COUNTRY: United States of America
ATORUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BEADABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: BEADABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: BASTICATION NUMBER: US/08/482,918
FILING DATE: 07-UNN-1995
CLASSIFICATION NUMBER: 36,107
RESISTANTION NUMBER: 36,107
RESISTANTION NUMBER: 36,107
RESISTANTION NUMBER: 36,107
RESISTANTION NUMBER: 312/474-6300
TELEPHONE: 312/474-6448
TELEPHONE: 312/474-6448
                                                 Query Match 100.0%; Score 1061; DB 2; Length 208; Best Local Similarity 100.0%; Pred. No. 3.4e-101; Matches 208; Conservative 0; Mismatches 0; Indels 0.
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100.0%; Score 1061; DB 2;
Best Local Similarity 100.0%; Pred. No. 3.4e-101;
Matches 208; Conservative 0; Mismatches 0;
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INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
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US-08-482-918-46
US-08-836-252A-6
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36,107
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                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
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Best Local Similarity
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US-336-728A-46

US-336-728A-46

US-336-728A-46

Sequence 46, Application US/08336728A

PERTENT NO. 6207802

GENERAL INFORMATION

APPLICANT: Bosselman, Robert A. APPLICANT: Besselman, Robert A. APPLICANT: Bosselman, Robert A. APPLICANT: Bosselman, Robert A. APPLICANT: Bosselman, Robert A. APPLICANT: Bosselman, Robert A. APPLICANT: Martin, Francis H. ITILE OF INVENTION: State Cell Factor NUMBERS OF SEQUENCES: 104

CORRESPONDENCE ADDRESS: 104

CORRESPONDENCE ADDRESS: 104

CORRESPONDENCE ADDRESS: 104

CORRESPONDENCE ADDRESS: 104

CORPUTER READBLE FORM:

MEDIN TYPE: Ploppy disk

COMPUTER READBLE FORM:

MEDIN TYPE: Ploppy disk

COMPUTER: DO-NOV-1994

FILING DATE: DO-NOV-1994

FILING DATE: DO-NOV-1994

FILING DATE: A-NOV-1990

FILING DATE: A-N
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SEQUENCE CHRARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-46
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEQLSNYSIIDKLVNIVDDLVECVKENSS 120
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CORRESPONDENCE ADDRESS:
STREEF Gas Marshall, O'Toole, Geretein, Murray & Borun STREET: Chicago
STREET: Chicago
STATE: 11linois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rclease #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/635,251
FILING DATE: 07-Aug-2000
CLASSIPICATION NUMBER: 08/449,182
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 08/172,329
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 08/172,329
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/684,535
FILING DATE: 01-OCT-1990
RILING DATE: 01-OCT-1990
APPLICATION NUMBER: 07/689,701
FILING DATE: 01-OCT-1990
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                                                                                                                                                                                                                                                                                                           Length 208;
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100.0%; Pred. No. 3.4e-101;
ative 0; Mismatches 0;
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; Patent No. 6759215
; GENERAL INFORMATION:
    APPLICANT: Zeebo, Krisztina M.
    Bosselman, Robert A.
    Suggs, Sidney V.
    Martin, Francis H.
    TITLE OF INVENTION: Stem Cell Factor
    NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 KPFMLPPVAASSLRNDSSSSNSKYIYLI 208
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    01017/32956
REFERENCE/DOCKET NUMBER: 0101
TELECOMMUNICATION INPORMATION:
TELEPHONE: 312/474-6300
TELEPK: 25-3856
INPORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acids
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121
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Best Local Similarity 100.0%; Pred. No. 3.4e-101;
Matches 208; Conservative 0; Mismatches 0; Indels 0
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-UN-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-COT-1899
ATTONEY/AGENT INFORMATION:
NAME: Clough, David W.
REFERENCE/DOCKET NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32957A
TELECOMMUNICATION INFORMATION:
TELEFRANIE: 312/474-648
TELEFRA: <University of TELEFRANIES TELEFRANIES TELEFRANIES
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
SEQUENCE TYPE: protein
SEQUENCE TYPE: protein
SEQUENCE TYPE: protein
SEQUENCE TYPE: protein
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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FILING DATE: 12-JAN-1998
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/49,653
CLASSIFICATION NUMBER: 07/982,255
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 07/589,701
PRIOR APPLICATION NUMBER: 07/589,701
PRIOR APPLICATION NUMBER: 07/589,701
PRIOR APPLICATION NUMBER: 07/573,616
PRIOR APPLICATION NUMBER: 07/573,616
PRIOR APPLICATION NUMBER: 07/573,616
PRIOR APPLICATION NUMBER: 07/537,198
PRIOR DATE: 11-JUN-1990
PRIOR APPLICATION NUMBER: 07/422,383
FILING DATE: 11-JUN-1990
PRIOR APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, DAYA!
REFERENCE/POCKET NUMBER: 36,107
REFERENCE/POCKET NUMBER: 36,107
REFERENCE/POCKET NUMBER: 01017/35136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 KPFMLPPVAASSLRNDSSSSNSKYIYLI 208
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INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 208 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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Matches 208; Conservative
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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Sequence 9, Application US/08628428

Sequence 9, Application US/08628428

Sequence 9, Application US/08628428

Sequence 9, Application US/08628428

GENERAL INFORMATION:

APPLICANT: Lu, Haieng
TITLE OF INVENTION:

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSE: Amgen Inc.

STREET: 1840 Delavilland Drive
CITY: Thousand Oaks
STATE: CA

COUNTRY: USA

ZIP: 91320-1789

CONDUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: THE PC compatible

COMPUTER: THE CC compatible

COMPUTER: THE PC COMPATA:

CURRENT APPLICATION DATA:
                                                                                  ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOCOMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,379B
FILING DATE: 28 MAR-1994
CLASSIFICATION: 435
                                      New York
: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 KPFMLPPVAASSLRNDSSSSNSK 203
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                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: CYCOM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: cleavage site LOCATION: 164..165
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                                      STATE: No COUNTRY:
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100.0%; Score 1061; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 3.4e-101;
Matches 208; Conservative 0; Mismatches 0; Indels 0
                                              COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPPY disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARR: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/604,325A

FILING DATE: 17-Jun-2002

APPLICATION NUMBER: 07/982,255

RILING DATE: 25-NOV-1992

APPLICATION NUMBER: 07/53,616

FILING DATE: 10-OCT-1990

APPLICATION NUMBER: 07/53,616

FILING DATE: 16-OCT-1990

APPLICATION NUMBER: 07/53,198

FILING DATE: 16-OCT-1990

APPLICATION NUMBER: 07/422,383

FILING DATE: 16-OCT-1999

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 31,107

REGISTRATION NUMBER: 01017/32953

TELEBERAX: 31,2/474-6300

TELEBERAX: 31,2/474-6300
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APPLICANT: No. 55.25708ka, Karl
APPLICANT: Lobell, Robert B
ATILE OF INVENTION: STABILIZED DIMER OF KIT LIGAND
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESSS:
ADDRESSES: Fish & Neave
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KPFMLPPVAASSLRNDSSSSNSKYIYLI 208
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
STATE: Illinois
COUNTRY: United States of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08220379B
Patent No. 5525708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-604-325A-46
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US-08-220-379B-2
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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Sequence 40. Application US/08482918
Fatent No. 6207417
GENERAL INFORMATION:
APPLICANT: Boselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
ITILE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                97.1%; Score 1030; DB 2; Length 273; 99.5%; Pred. No. 7.9e-98; tive 0; Mismatches 1; Indels
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                    REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-0448
TELEFAX: 312/474-0448
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
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STATE: 111inois
COUNTRY: United States of America
ZIP: 6060-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, DAVIG W.
REGISTRATION NUMBER: 36,1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 KPFMLPPVAASSLRNDSSSSNSK 203
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 99.5'
Matches 202; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-482-918-48
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US-08-482-918-49
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1-248 SCF protein begins at amino acid 26; amino acid 1-25
include Met and leader sequences for membrane band form of
recombinant SCF."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKOFVVASETSDCVVSSTLSPEKOSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKKTQTWILTCIYLQILLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKKTOTWILTCIYLOLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
97.1%; Score 1030; DB 1; Length 273;
Best Local Similarity 99.5%; Pred. No. 7.9e-98;
Matches 202; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 48, Application US/08482918
Patent No. 6207417
GENERAL INFORMATION:
APPLICANT: Zesbo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
APPLICATION NUMBER: US/08/628,428
CIASSIPTCATION: 435
CIASSIPTCATION: 435
ATTORNEY ABENT INFORMATION:
NAME: Knight, Matthew W
REGISTRATION NUMBER: 36,846
REGISTRATION NUMBER: 36,846
REGISTRATION NUMBER: 36,846
REGISTRATION NOW 9:
REPRENCE/DOCKET NUMBER: A-400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 KPFMLPPVAASSLRNDSSSSNSK 203
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ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Protein
LOCATION: 1.273
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                                                                                                                                                    121 KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
APPLICANT: Zeebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Bosselman, Robert A.
APPLICANT: Martin, Francis H.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STRERT: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: 111inois STATE: 111inois COUNTY: United States of America ZIP: 60606-6402 COMPUTER READABLE FORM: WEDJUM TYPE: Floppy disk COMPUTER: Plan PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION DATA:
PRICK APPLICATION DATA:
PRICK APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRICK APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRICK APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 25-NOV-1992
PRICK APPLICATION DATA:
APPLICATION NUMBER: 07/539,616
FILING DATE: 24-AUG-1990
PRICK APPLICATION DATA:
APPLICATION NUMBER: 07/533,198
FILING DATE: 11-JUN-1990
PRICK APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRICK APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
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REGISTRATION NUMBER: 36,107
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US-09-224-681-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKKTQTWILTCIYLQLLLENPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                                                                                                                                                                                                                                                                                                                                                        1 MKKTQTWILICIYLQLLLPNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
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APPLICANT: Suggs, Sidney V.
APPLICANT: Bosselman, Robert A.
APPLICANT: Buggs, Sidney V.
APPLICANT: Busselman, Robert A.
APPLICANT: Busselman, Robert A.
APPLICANT: Bustel, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS: 104
CORRESPONDENCE ADDRESS: 104
CORRESPONDENCE ADDRESS: Marthall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 6060-6402
COMPUTER READBLE FORM:
MEDIUM TYPE: RIOPPRY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE FORM:
COMPATIBLE FOR
                                                                                                                                                                                                                                Query Match 97.1%; Score 1030; DB 2; Length 273; Best Local Similarity 99.5%; Pred. No. 7.9e-98; Matches 202; Conservative 0; Mismatches 1; Indels
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SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATYORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFRENCE/DOCKET NUMBER: 01017/33005
TELEPOMMUNICATION INFORMATION:
TELEPOMMUNICATION INFORMATION:
TELEPOMMUNICATION INFORMATION:
TELEPOMMUNICATION INFORMATION:
TELEPOMMUNICATION 1970-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 KPFMLPPVAASSLRNDSSSSNRK 203
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Patent No. 6207417
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 273 amino acids
amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                    TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-482-918-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-08-482-918-61
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Fatent No. 6207454

GENERAL INFORMATION:
APPLICANT: Seebo, Krisztina M.
APPLICANT: Suespelman, Robert A.
APPLICANT: Suespelman, Robert A.
APPLICANT: Suespelman, Robert A.
APPLICANT: Bosselman, Robert A.
APPLICANT: Martin, Francis H.
ITILE OF INVENTION: Method for Enhancing the Efficiency of Gene TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: Gloud Sears Tower, 233 South Wacker Drive CITY: Chicago
CITY: Chicago
STRATE: Illinois
COUNTRY: United States of America
ZIP: 6666-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: LBM PC Compatible
COMPUTER: LBM PC Compatible
COMPUTER: LBM PC Compatible
COMPUTER: LBM PC Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
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                                                                                                                                                                                                                                                                                          Query Match 97.1%; Score 1030; DB 2; Best Local Similarity 99.5%; Pred. No. 7.9e-98; Matches 202; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 KPFMLPPVAASSLRNDSSSSNSK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                      TELEX:
INFORMATION FOR SEQ ID NO: 48
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                            MOLECULE TYPE: protein US-09-224-681-48
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MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KOLKKSFKSPEPRLFTPREFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
APPLICANT: Zeebo, Krisztina M.
APPLICANT: Seebo, Krisztina M.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Transfer With Stem Cell Factor (SCF) Polypeptide NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: Giolo Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION NUMBER: 07/422,383
FILING DATE: 11-OUN-1990
PRIOR APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 36,107
REPRENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KPFMLPPVAASSLRNDSSSSNRK 203
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Patent No. 6207454
                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 499
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.5
Matches 202, Conservative
                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-49
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CURRENT APPLICATION DATA:

FILING DATE:

CLASSIFICATION:

FRIDA APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: 09/05,893

FILING DATE: 12-NNV-1995

FILING DATE: 24-NNV-1995

FILING DATE: 25-NNV-1995

FILING DATE: 25-NNV-1992

FRIDA APPLICATION DATA:

APPLICATION NUMBER: 07/882,255

FILING DATE: 25-NNV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/589,701

FILING DATE: 25-NNV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/537,198

FILING DATE: 24-NNV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/237,198

FILING DATE: 11-JUN-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/237,198

FILING DATE: 11-JUN-1990

PRIOR APPLICATION NUMBER: 07/237,198

FILING DATE: 11-JUN-1990

PRIOR APPLICATION NUMBER: 07/437,198

FILING DATE: 11-JUN-1990

FILING DATE: 13-1744-6300

FILENCHING DATE: 13-12/44-488

FILECOMMUNICATION INCRRAFICE:

REFERMING CHARACTERISTICS:

LENGTH: 273 amino acids

TYDEDCOMMUNICATION INCRRAFICE:

1 TYPER: amino acid

1 TYPE: TPE: PFOCECIN

WOLLECTIE: 19PE: PFOCECIN

UG-09-224-681-61-61-
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 Query Match
 97.1%;
 Score 1030;
 DB 2;
 Length 273;

 Best Local Similarity 99.5%;
 Pred. No. 7.9e-98;
 Indels 0;
 Gaps 0;

 Matches 202;
 Conservative 0;
 Mismatches 1;
 Indels 0;
 Gaps 0;

 Qy
 IMEXTOTWILTCIXLOLLENDLYKTEGICRNRYTRNVKDVTKLVANLPKDYMITLKXVPG 60
 INDELSTANTICIXLOLLENDLYKTEGICRNRYTRNVKDVTKLVANLPKDYMITLKXVPG 60

 Db
 1 MEXTOTWILTCIXLOLLENDLYKTEGICRNRYTRNVKDVTKLVANLPKDYMITLKXVPG 60

 CQ
 61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISGISNYSIIDKLVNIVDDLYCYKRNSS 120

 Db
 61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISGISNYSIIDKLVNIVDDLYCVKRNSS 120

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Search completed: February 22, 2006, 18:21:58 Job time : 26.2121 secs

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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
TLING DATE: 24-MAY-1995
CLASSIFICATION NUMBER: 08/449,653
FILING DATE: 25-MOV-1995
FILING DATE: 25-MOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/53,616
FILING DATE: 24-MUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/53,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, DAVIGM:
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 36,107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                   US-09-005-243-46
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1061
1 MKKTQTWILTCIYLQLLLFN......AASSLRNDSSSSNSKYIYLI
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(cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*)
5.1.7
Biocceleration Ltd
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US-09-224-683-46
US-10-620-642-46
US-09-005-243-48
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US-09-224-683-49
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US-10-620-642-57
US-09-224-683-57
US-09-224-683-53
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 GenCore version (c) 1993 - 2006
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Maximum Match 100%
Listing first 45 summaries
                                      OM protein - protein search, using sw model
                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Sequence Seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Marchall, O'Toole, Gerstein, Murray & BTREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: 111inois COUNTRY: United States of America ZIP: 60606-6402 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/005,243
US-10-688-845-87

US-10-620-642-63

US-09-005-234-683-52

US-10-175-608-52

US-10-620-642-52

US-10-175-608-53

US-09-224-683-53

US-10-620-642-53

US-09-224-683-53

US-09-224-683-53

US-09-005-243-44

US-09-005-243-64

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Fatent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
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TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1061; DB 3; Length 208; 100.0%; Pred. No. 7.6e-92; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: 11linois COUWRY: United States of America ZIP: 60606-6402 CONPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: Ploppy disk COMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 46, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
GREACH Seabo, Kristina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Sugge, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 KPFMLPPVAASSLRNDSSSSNSKYIYLI 208
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 208; Conservative
                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-09-005-243-46
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US-09-224-683-46
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: 11linois
COUNTRY: United States of America
ZIP: 606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/175,608
FILING DATE: 16-Oct-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 1061; DB 3; Length 208; Best Local Similarity 100.0%; Pred. No. 7.6e-92; Matches 208; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KPFMLPPVAASSLRNDSSSSNSKYIYLI 208
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                                                                                                                                                                                                                                                                                                                                              01017/35136
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-UJN-1990
PRIOR APPLICATION NUMBER: 07/422,383
PRILING DATE: 11-COT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clugh, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 36,107
TELEPHONE: 312/474-6300
TELEFPANE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 46, Application US/10175608
Publication No. US20040181044A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
Bosselman, Robert A.
Suggs, Sidney V.
                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 208 amino acids
amino acid
GY: linear
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 KOLKKSFKSPEPRLFTPREFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
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                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1061; DB 5;
100.0%; Pred. No. 7.6e-92;
iive 0; Mismatches 0;
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STATE: Illinois
COUNTRY: United States of America
                                                                                                                                                                                                  APPLICATION NUMBER: US/10/620,642
FILING DATE: 16-Jul-2003
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/175,608
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 09/635,249
FILING DATE: 16-OCC-2002
APPLICATION NUMBER: 09/635,249
FILING DATE: 07-AUG-2002
APPLICATION NUMBER: 09/466,546
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 07/982,255
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/64,535
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/64,535
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/573,616
FILING DATE: 11-UDN-1990
APPLICATION NUMBER: 07/573,198
FILING DATE: 11-UN-1990
APPLICATION NUMBER: 07/573,198
FILING DATE: 11-UN-1990
APPLICATION NUMBER: 07/52,383
FILING DATE: 11-UN-1990
APPLICATION NUMBER: 07/52,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGRY INFORMATION:
NAME: Clough, David W.
REFERENCE/DOCKET NUMBER: 01017/35
TELECOMMUNICATION INFORMATION:
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-10-620-642-46
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INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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Best Local Similarity 100.
Matches 208; Conservative
                                           ZIP: 60606-6402
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US-09-005-243-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KULKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKXVPG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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Best Local Similarity 100.0%; Pred. No. 7.6e-92;
Matches 208; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01017/35199
                                                                                                                                                                                                                                           FILING DATE: 10-APR-1991
APPLICATION NUMBER: 09/589,701
FILING DATE: 10-OCT-1991
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/573,198
FILING DATE: 11-UUN-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
                                                              FILING DATE: 07-AUG-2000
APPLICATION NUMBER: 09/486,546
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 08/172,329
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
APPLICATION NUMBER: 07/684,535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
                                              APPLICATION NUMBER: 09/635,249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
  CLASSIFICATION: <U
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Chicago
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US-10-620-642-46
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Sequence 49, Application US/09005243
; Patent No. US20020018763A1
; GENERALINFORMATION:
; APPLICANT: Zebo, Krisztina M.
APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marchall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Chicago
COUTRY: United States of America
COUTRY: United States of America
CONTRY: United States of America
CONTRY: United States of America
CONTRY: United States of America
CONFUTER: Inhinois
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE: 25-NOV-1995
CLASSIFICATION NUMBER: 08/449,653
APPLICATION NUMBER: 07/589,701
RELING DATE: 25-NOV-1995
FILING DATE: 24-ANG-1990
RELOR APPLICATION NUMBER: 01-OCT-1990
RELOR APPLICATION NUMBER: 01-OCT-1990
RELOR APPLICATION NUMBER: 01-OCT-1989
ATTING DATE: 14-AUG-1990
RELOR APPLICATION NUMBER: 36,107
REGISTRATION NUMBER: 36,107
REGISTRATION NUMBER: 36,107
REGISTRATION NUMBER: 36,107
REGISTRATION NUMBER: 312/474-6048
TELEERAK: 312/474-6448
TELEERAK: 312/474-0448
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                                                                                                               181 KPFMLPPVAASSLRNDSSSSNSK 203
                                                                                                                                              181 KPFMLPPVAASSLRNDSSSSNRK 203
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INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
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MOLECULE TYPE: protein
US-09-005-243-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
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Best Local Similarity
                                                                                                                                                                                                                                                     RESULT 6
US-09-005-243-49
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Sequence 49, Application US/09005243

Patent No. US200200187531

GENERAL INFORMATION

APPLICANT: Seabo, Kriaztina M.
APPLICANT: Seabo, Kriaztina M.
APPLICANT: Seabo, Kriaztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Borge Science of America CITT: CANTE: United Sears Tower, 233 South Wacker Drive CITT: Chicago
CITT: Chicago
CONTRE: United Sears Tower, 233 South Wacker Drive CITT: Chicago
CONTRE: Lilindo Sears Tower, 233 South Wacker Drive CITT: Chicago
CONTRE: Lilindo Sears Tower, 233 South Wacker Drive CITT: Chicago
CONTRESEE: Rear Proper distance of America CONTRE: Lilindo Sears Tower, 233 South Wacker Drive CONTRESEE: Rear Proper distance of America CONTRESEE: Lilindo Sears Tower, 233 South Wacker CONTRESEE: Rear Proper distance of America CONTRESEE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/005,443
FILING DATE: 25-WOV-1992
APPLICATION NUMBER: 07/589,701
FILING DATE: 25-WOV-1992
APPLICATION NUMBER: 07/53,198
FILING DATE: 25-WOV-1990
PRIOR APPLICATION NUMBER: 07/53,198
FILING DATE: 11-UN-1990
PRIOR APPLICATION NUMBER: 07/422,383
FILING DATE: 11-UN-1990
PRIOR APPLICATION NUMBER: 07/44048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 97.1%; Score 1030; DB 3; Length 273; Best Local Similarity 99.5%; Pred. No. 9.2e-89; Matches 202; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-005-243-48
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKKTQTWILITCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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                                                                                                                                                                                                                                                                       Score 1030; DB 3;
Pred. No. 9.2e-89;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 KPFMLPPVAASSLRNDSSSSNRK 203
                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 99.5%;
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                               Matches 202; Conservative
                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-005-243-61
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US-09-224-683-48
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                                                                                                                                                                                                                                                                                                                                               61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                        1 MKKTQTWILITCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                                    1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENES S.

CORRESPONDENCE ADDRESS:
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: 111inois
COUNTRY: United States of America
ZIP: 6066-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 07/593,616
FILING DATE: 07/593,198
FILING DATE: 11-UW-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/523,383
FILING DATE: 11-UW-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/523,198
FILING DATE: 11-UW-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/523,198
FILING DATE: 11-UW-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/523,198
FILING DATE: 11-UW-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/503,198
FILING DATE: 11-UW-1990
PRIOR APPLICATION NUMBER: 07/503,198
   1; Indels
   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 61, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Buggs, Sidney V.
APPLICANT: Martin, Francis H.
TILLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
IELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 KPFMLPPVAASSLRNDSSSSNSK 203
Matches 202; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 312/474-0448
TELEX: 25-3856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVBCVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKKTQTWILICIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKKTQTWILICIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
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| Sequence 49, Application US/09224683
| Patent No. US20020031491A1 |
| CENERAL INFORMATION: APPLICANT: Zeebo, Krisztina M. |
| APPLICANT: Suggs, Sidney V. |
| APPLICANT: Martin, Francis H. |
| TITLE OF INVENTION: Stem Cell Factor: Composition Claims NUMBER OF SEQUENCES: 104 |
| CORRESPONDENCE ADDRESS: 106 |
| CORRESPONDENCE ADDRESS: 107 |
| CONTINCE Illinois |
| COUNTRY: United States of America |
| COMPUTER READABLE FORM: |
| MEDIUM TYPE: Floppy disk |
| COMPUTER: IBM PC compatible |
| COMPUTER: APPLICATION NUMBER: US/09/224,683 |
| FILING DATE: COMPUTER: COM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 97.1%; Score 1030; DB 3; Length 273; Best Local Similarity 99.5%; Pred. No. 9.2e-89; Matches 202; Conservative 0; Mismatches 1; Indels
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-UNN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-CCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEPAX: 0.000
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-224-683-48
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US-09-224-683-49
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121 KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
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Patent No. US20020031491A1

GENERAL INPORMATION:
APPLICANT: Zeebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: G3100 Sears Tower, 233 South Wacker Drive
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 97.1%; Score 1030; DB 3; Length 273; Best Local Similarity 99.5%; Pred. No. 9.2e-89; Matches 202; Conservative 0; Mismatches 1; Indels (
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION NUMBER: 07/573,198
FILING DATE: 24-AUG-1990
PRIOR APPLICATION NUMBER: 07/52,383
FILING DATE: 11-JUN-1990
PRIOR APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1990
PRIOR APPLICATION NUMBER: 01/735
FILING DATE: 16-OCT-1999
PRIOR APPLICATION NUMBER: 01/735
FILING DATE: 16-OCT-1999
PRIOR APPLICATION NUMBER: 01017/35
FILING DATE: 312/474-0418
TELEFAM: 312/474-0418
FILICATION NUMBER: 01017/35
FILICATI
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MOLECULE TYPE: protein
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US-10-175-608-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 KDLKKSPRSPEPRLFTPBEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKKTQTWILLCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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                                                          COMPUTER: BLADELE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 24-MG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 11-CT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 11-CCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/53,198
FILING DATE: 11-CCT-1989
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,107
REBERRENCE/OFFORTION NUMBER: 36,107
REGISTRATION NUMBER: 36,107
RELEPAN: 312/474-6448
TELEFRAN: 312/474-6448
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-09-224-683-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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KPFMLPPVAASSLRNDSSSSNRK 203

181

RESULT 11

1 MKKTQTWILTCIYLQLLEFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG Gaps Sequence 48, Application US/10175608
Publication No. US20040181044A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive ô Query Match 97.1%; Score 1030; DB 4; Length 273; Best Local Similarity 99.5%; Pred. No. 9.2e-89; Matches 202; Conservative 0; Mismatches 1; Indels NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMUNICATION INFORMATION:
TELEPHONE: 312/474-6300 ;
TOPOLOGY: linear
;
MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-10-175-608-48 SEQUENCE CHARACTERISTICS: LENGTH: 273 amino acids TYPE: amino acid TELEFAX: 312/474-0448 INFORMATION FOR SEQ ID NO: 48: TELEX: <Unknown> 61 61 셤 ઠે g

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RESULT 13
US-10-175-608-61
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                             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Chicago
CITY: Chicago
STATE: 111inois
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Plopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/175,608
FILING DATE: 16-Oct-2002
APPLICATION NUMBER: 09/486,546
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 09/486,546
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/684,535
APPLICATION NUMBER: 07/684,535
FILING DATE: 10-OCT-1991
APPLICATION NUMBER: 07/64,535
FILING DATE: 10-OCT-1991
APPLICATION NUMBER: 07/42,383
FILING DATE: 10-OCT-1991
APPLICATION NUMBER: 07/422,383
FILING DATE: 11-UN-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 11-OCT-1989
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 01017/35199
TELEROMUNICATION INFORMATION:
REGISTRATION NUMBER: 01017/35199
TELEROMUNICATION INFORMATION:
FELENCHMUNICATION INFORMATION:
TELEROMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
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; SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-175-608-49
                                                                                                                                   181 KPFMLPPVAASSLRNDSSSSNRK 203
                                                                                                   KPFMLPPVAASSLRNDSSSSNSK 203
                                                                                                                                                                                                                            RESULT 12
US-10-175-608-49
; Sequence 49, Application US/10175608
; Publication No. US20040181044A1
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
121
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1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                                                                                                                                                                               61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                       1 MKKTQTWILITCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                                                                                                                                                                                                                                                                                        KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKOFVVASETSOCVVSSTLSPEKOSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                   61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago
                                                       .;
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     Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER: Rebable FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IS PR PC compatible DOS

SOFTWARE: PATENT: PC-DOS/MS-DOS

SOFTWARE: PATENT: No. Version #1.30

CURRENT APPLICATION NUMBER: US/10/175,608

FILING DATE: 16-Oct-2002

CLASSIFICATION NUMBER: 09/635,249

FILING DATE: 07-AUG-2000

APPLICATION NUMBER: 09/486,546

FILING DATE: 20-NOV-1995

APPLICATION NUMBER: 08/172,329

FILING DATE: 25-NOV-1995

APPLICATION NUMBER: 09/88,535

FILING DATE: 10-APR-1991

APPLICATION NUMBER: 09/589,701

FILING DATE: 10-APR-1991

APPLICATION NUMBER: 09/589,701

FILING DATE: 10-APR-1991

APPLICATION NUMBER: 07/53,616

FILING DATE: 24-AUG-1990

APPLICATION NUMBER: 07/53,198

FILING DATE: 11-JUN-1990

APPLICATION NUMBER: 07/53,198

FILING DATE: 11-JUN-1990

APPLICATION NUMBER: 07/422,383
                                                       1; Indels
  Score 1030; DB 4;
Pred. No. 9.2e-89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
Query Match
97.1%; Score 1030; D.
Best Local Similarity 99.5%; Pred. No. 9.2e
Matches 202; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 KPFMLPPVAASSLRNDSSSSNSK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 61, Application US/10175608; Publication No. US20040181044A1; GENEBAL INFORMATION: APPLICANT: Zsebo, Krisztina M.
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKPSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
61 MDVLPSHCWISEMVVQLSDSLTDLLDKPSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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US-10-620-642-49

i Sequence 49, Application US/10620642

i Sequence 49, Application US/10620642

i Sequence 49, Application No. US20050080250A1

i GENERAL INFORMATION:
BOSSELMAN, Robert A.
BOSSELMAN, Francis H.

ITILE OF INVENTION: Stem Cell Pactor

NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESSE:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Lilinois
STATE: Illinois
COUNTRY: United States of America
ZIP: 6666-6402
COMPUTER: READBLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIALE
COMPUTER: PROPER: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/620,642
FILING DATE: 16-Jul-2003
CLASSIFICATION: <Unknown>
                                                                                                     AFFLICATION NUMBER: 07/502, 101

PILING DATE: 10-OCT-1991

PILING DATE: 10-OCT-1991

APPLICATION NUMBER: 07/573,616

PILING DATE: 11-JUN-1990

APPLICATION NUMBER: 07/422,383

PILING DATE: 11-JUN-1990

ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107

REGISTRATION NUMBER: 36,107

RELEPHONE: 312/474-6300

TELEPHONE: 312/474-6300

TELERAX: 312/474-6300

TELERX: <UNKNOWN:
TELEX: <UNKNOWN:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids

TYPE: amino acids

TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-10-620-642-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 KPFMLPPVAASSLRNDSSSSNRK 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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CORRESPONDENCE ADDRESS:
CORRESPONDENCE Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago
STREET: 11linoid States of America
ZITE: 60666-6402
COMPUTER READABLE Floppy disk
COMPUTER READABLE PLOPPY disk
COMPUTER: BM PC Compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAPLICATION DATA:
APPLICATION NUMBER: US/10/620,642
FILING DATE: 16-U1-2003
APPLICATION NUMBER: US/10/175,608
FILING DATE: 16-Oct-2002
APPLICATION NUMBER: US/10/175,608
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 09/486,546
FILING DATE: 24-MAY-1993
APPLICATION NUMBER: 09/486,546
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 09/486,546
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 09/486,546
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 09/486,535
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/982,255
FILING DATE: 10-APR-1991
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                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 61:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 KPFMLPPVAASSLRNDSSSSNRK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KPFMLPPVAASSLRNDSSSSNSK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 48, Application US/10620642
Publication No. US20050080250A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
                                                                                       TELEPHONE: 312/474-6300
                                                                                                                                                                                                    LENGTH: 273 amino acids TYPE: amino acid
                                                                                                          TELEFAX: 312/474-0448
TELEX: «Unchrown»
INFORWATION FOR SEQ ID 00: 61:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                      US-10-175-608-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-620-642-48
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Gaps

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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/10/175,608

APILING DATE: 16-OCt-2002

APPLICATION NUMBER: 09/635,249

FILING DATE: 07-AUG-2000

APPLICATION NUMBER: 09/486,546

FILING DATE: 24-MAY-1995

APPLICATION NUMBER: 06/172,329

FILING DATE: 21-DEC-1993

APPLICATION NUMBER: 07/684,255

FILING DATE: 10-APR-1991

APPLICATION NUMBER: 07/684,535

FILING DATE: 10-APR-1991

APPLICATION NUMBER: 07/53,616

FILING DATE: 10-OCT-1991

APPLICATION NUMBER: 07/53,198

FILING DATE: 10-OCT-1990

APPLICATION NUMBER: 07/53,198

FILING DATE: 16-OCT-1990

APPLICATION NUMBER: 07/53,198

FILING DATE: 16-OCT-1990

APPLICATION NUMBER: 07/53,383

FILING DATE: 16-OCT-1999

ATTORNEY AGENT INFORMATION:

NAME: CLOUGH, DAVIG N.

REGISTRATION NUMBER: 36,107

TELECOMMUNICATION INFORMATION:

TELEFRANCE JAZ-474-6300

TELEFRANCE JAZ-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-620-642-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 KPFMLPPVAASSLRNDSSSSNSK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 KPFMLPPVAASSLRNDSSSSNRK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: <UNKNOWN>
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
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UD 181 KFFMLFVAASSLKNUSSSSNKK 203 Search completed: February 22, 2006, 18:26:55 Job time : 84.0854 8ecs

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RESULT 1
US-10-353-783-46
46, Appl
61, Appl
61, Appl
50, Appl
24, Appl
226, App
520, App
520, App
529, App
529, App
529, App
538, App
500, App
501, App
511, App
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                                                                                                                                 February 22, 2006, 18:22:17; Search time 8.02204 Seconds (without alignments) 386.005 Million cell updates/sec
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                                                                                                                                                                                                               US-10-620-642-46
1061
1 MKKTQTWILTCIYLQLLLFN......AASSLRNDSSSSNSKYIYLI 208
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1: /cgn2_6/ptodata/2/pubpaa/USOB NEW PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USOB.NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
                    5.1.7
Biocceleration Ltd.
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US-10-353-783-48
US-10-353-783-49
US-10-353-783-61
US-10-353-783-50
US-10-353-783-51
US-10-353-783-57
US-11-176-830-520
US-11-176-830-539
US-11-176-830-539
US-11-176-830-539
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                    version -
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Maximum Match 100%
Listing first 45 summaries
                                                                                                sw model
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Gapop 10.0 , Gapext 0.5
                    GenCore (c) 1993
                                                                                              protein search, using
                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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                                                                                              OM protein
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Publication No. US2005261175A1

Publication No. US20052651175A1

Publication No. US20052651175A1

Bosselman, Robert A.

Suggs, Sidney V.

WHATIO, Francis H.

TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104

CONRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borunger OF SEQUENCES: 104

CONNESSER: Marshall, O'Toole, Gerstein, Murray & Borunger STATE: Illinois

COUWTRY: United States of America

TITLE OF INVENTION: Stem Cell Factor

COMPUTER READALE FORD:
COMPUTER PAPELICATION DATA:
APPLICATION NUMBER: 03/10/353,783

FILING DATE: 21-DE-1995

APPLICATION NUMBER: 07/593,516

FILING DATE: 10-CT-1990

APPLICATION NUMBER: 07/593,108

FILING DATE: 11-JUN-1990

APPLICATION NUMBER: 07/593,108

FILING DATE: 11-JUN-1990

APPLICATION NUMBER: 07/537,108

FILING DATE: 10-CT-1990

APPLICATION NUMBER: 07/537,108

FILING DATE: 10-CM-1990

APPLICATION NUMBER: 07/537,108

FILING DATE: 00-CM-1990

APPLICATION NUMBER: 07/537,108

FILING DATE: 00-CM-1990

APPLICATION NUMBER: 07/537,108

FILING DATE: 00-CM-1090

APPLICATION NUMBER: 07/53
US-11-176-830-508
US-11-176-830-510
US-11-176-830-512
US-11-176-830-512
US-11-176-830-522
US-11-176-830-522
US-11-176-830-523
US-11-176-830-531
US-11-176-830-534
US-11-176-830-534
US-11-176-830-534
US-11-176-830-542
US-11-176-830-505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKPSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KOLKKSPKSPEPRLFTPBEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKKTQTWILTCIYLQLLLENPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMILKYVPG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 6006-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Parentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32958A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.1%; Score 1030; DB 6;
99.5%; Pred. No. 7.5e-86;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/10/353,783
FILING DATE: 28-Jan-2003
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION WUMBER: 08/448,729
FILING DATE: 24-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KPFMLPPVAASSLRNDSSSSNRK 203
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Publication No. USZ0050261175A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
                                                                                                                                                                                                                                                   TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 273 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                            TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 99.5
Matches 202, Conservative
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US-10-353-783-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKKTQTWILTCIYLQLLLFNPLVKTBGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: 111inois COUNTRY: United States of America ZIP: 6606-6402 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPUTER: DAY PC COMPUTIBLE: DAY PC COMPUTIBLE: PLOSS SOFTWARE: PATENTIN Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                             Length 208;
                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                             DB 6;
                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 1061; DB 6; Best Local Similarity 100.0%; Pred. No. 8.5e-89; Matches 208; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/353,783
FILING DATE: 28-Jan-2003
CLASSIFTCATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/448,729
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 08/172,329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 KPFMLPPVAASSLRNDSSSSNSKYIYLI 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
                                                                                                                                                                           ; TOPOLOGY: linear; ; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 46: US-10-353-783-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 25-NOV-1992
APPLICATION WUMBER: 07/684,535
APLICATION DATE: 10-APR-1991
APPLICATION NUMBER: 07/589,701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/982,255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 07/573,616
  TELECOMMUNICATION INFORMATION:
TELEFAX: 312/474-6300
TELEFAX: 312/474-0448
TELEX: cUnknown:
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 48, Application US/10353783
Publication No. US2050261175A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS
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US-10-353-783-48
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61 MDVLPSHCWISEMVVQLSDSLTDLLDXFSNISECLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKKTQTWILICIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 273;
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                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.1%; Score 1030; DB 6;
99.5%; Pred. No. 7.5e-86;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32958A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/448,729
FILING DATE: 24-MX-1995
APPLICATION NUMBER: 08/172,329
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/882,255
FILING DATE: 25-MOV-1992
APPLICATION NUMBER: 07/884,535
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/589,701
FILING DATE: 10-OCT-1990
APPLICATION NUMBER: 07/573,616
FILING DATE: 10-OCT-1990
APPLICATION NUMBER: 07/573,198
FILING DATE: 11-UNU-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-UNU-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 11-ON-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/353,783
FILING DATE: 28-Jan-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 61:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 KPFMLPPVAASSLRNDSSSSNRK 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 50, Application US/10353783
; Publication No. US20650261175A1
; GENEBLI INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 273 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.5;
Matches 202; Conservative
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US-10-353-783-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKOFVVASBTSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKKTQTWILTCIYLQLLLENPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 97.1%; Score 1030; DB 6; Length 273; Best Local Similarity 99.5%; Pred. No. 7.5e-86; Matches 202; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INPORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32958A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 61, Application US/10353783;
Publication No. US20050261175A1
GENERAL INFORMATION: Krisztina M.
APPLICANT: Zeebo, Krisztina M.
Boseelman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                     APPLICATION NUMBER: 07/684,535
APPLICATION NUMBER: 07/684,535
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-CCT-1990
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/573,198
FILING DATE: 11-UNN-1990
APPLICATION NUMBER: 07/523,383
FILING DATE: 16-CCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: protein
US-10-353-783-49
               FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/982,255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 KPFMLPPVAASSLRNDSSSSNRK 203
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INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acid
TYPE: amino acid
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TELEFAX: 312/474-0448
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US-10-353-783-61
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
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                                                                  STATE: Illinois
CUNTRY: United States of America
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Tal PC COMPATIBLE
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/353,783
FILING DATE: 28-Jan-2003
CLASSIFICATION: CUNKNOWn>
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APPLICATION DATA:

APPLICATION NUMBER: 08/448,729

FILING DATE: 24-MAX-1995

APPLICATION NUMBER: 08/172,329

FILING DATE: 21-DEC-1993

APPLICATION NUMBER: 07/684,535

FILING DATE: 02-NOV-1992

APPLICATION NUMBER: 07/684,535

FILING DATE: 01-OCT-1990

APPLICATION NUMBER: 07/589,701

FILING DATE: 01-OCT-1990

APPLICATION NUMBER: 07/53,616

FILING DATE: 10-OCT-1990

APPLICATION NUMBER: 07/53,198

FILING DATE: 11-0TN-1990

APPLICATION NUMBER: 07/432,383

FILING DATE: 16-OCT-1989

ATTORREY/AGENT: INFORMATION:

REGISTRATION NUMBER: 36,107

REGISTRATION NUMBER: 36,107

REGISTRATION NUMBER: 36,107

REGISTRATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear;
HOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-10-353-783-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 KPFMLPPVAASSLRNDSSSSNRK 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
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MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                            Martin, Francis H.

TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
RADBRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRIT APPLICATION DATA:
APPLICATION NUMBER: US/10/353,783
FILING DATE: 28-Jan-2003
CLASSIPICATION: CUNKNOWN>
PRIOR APPLICATION: ON WINDER: 08/448,729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 920; DB Pred. No. 6e-767; Mismatches
                                                                                                                                                                                                                                                                                                                STATE: Illinois
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 08/172,329
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
APPLICATION NUMBER: 07/684,535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/589, 701
FILING DATE: 01-OCT-1990
APPLICATION NUMBER: 07/573, 616
FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/537, 198
FILING DATE: 11-UN-1990
APPLICATION NUMBER: 07/422, 383
FILING DATE: 16-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
Sequence 57, Application US/10353783
Publication No. US20050261175A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
Bosselman, Robert A.
Suggs, Sidney V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 266 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86.7%;
92.6%;
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 92.6
Matches 188; Conservative
                                                                                                                                                                                                                                                                                             CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-353-783-57
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Sequence 520, Application US/11176830

Substitution No. US20060020116A1

GENERAL INFORMATION:

APPLICANT: Gantier, Rene

APPLICANT: Gantier, Rene

APPLICANT: Gantier, Rene

APPLICANT: Drittanti, Lila

APPLICANT: Vega, Manuel

ITILE OF INVENTION: Acid Molecules and Related Applications

TITLE OF INVENTION: Acid Molecules and Related Applications

CURRENT APPLICATION NUMBER: US/11/176,830

CURRENT FILING DATE: 2003-09-08

PRIOR APPLICATION NUMBER: 60/457,135

PRIOR APPLICATION NUMBER: 60/409,898

PRIOR APPLICATION NUMBER: 60/409,898

PRIOR APPLICATION NUMBER: 2003-09-09

NUMBER OF SEQ ID NOS: 1306

SEQ ID NO 520

LENGTH: 248

PRIOR PLING DATE: 2003-09-09

NUMBER: DEBAGGE FOR WINDOWS VERSION 4.0

SEQ ID NO 520

LENGTH: 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 DKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSSKDLKKSFKSPEPRLFTPEEFFRIFN 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 RSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVTKPFMLPPVAASSLRNDSSSSNRK 178
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                                                                                                                                                                                                                                                                                                                                                         Score 898; DB 7; Length 248;
Pred. No. 5.3e-74;
                                                                                                                                                                                                                                                                                                                                     94.6%; Sco...
99.4%; Pred. No. s...
0; Mismatches
                                                                                                                                                           TYPE: PRT
CRGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank AAA85450
STATABASE RNTRY DATE: 1996-01-19
US-11-176-830-206
PRIOR APPLICATION NUMBER: 60/409,898
PRIOR FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SOPTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 206
LENGTH: 248
                                                                                                                                                                                                                                                                                                                                                                                                               Matches 177; Conservative
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Matches 176; Conservative
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US-11-176-830-520
                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                           APPLICANT: LEE, Hak-Bup
APPLICANT: LIS, Hak-Bup
APPLICANT: LIS, Hak-Bup
APPLICANT: KIM, Jae-Youn
APPLICANT: KIM, Jae-Youn
TITLE OF INVENTION: A method of improving efficacy of biological response-modifying
TITLE OF INVENTION: Droteins and the example muteins
TITLE OF INVENTION: Droteins and the example muteins
TITLE OF INVENTION: Droteins and the example muteins
TITLE OF INVENTION WIMBER: US/10/519,390
CURRENT APPLICATION NUMBER: KR10-2003-0051846
PRIOR FILING DATE: 2003-07-26
NUMBER OF SEQ ID NOS: 65
SEQ ID NOS: 65
SEQ ID NO 24
LENGTH: 248
TYPE: NUMBER: NO 24
TYPE: NO 24
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Publication No. US20060020116A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Guyon, Thierry
APPLICANT: Guyon, Thierry
APPLICANT: Drittanti, Lila
APPLICANT: Vega, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding N
TITLE OF INVENTION: Acid Molecules and Related Applications
FILE REPREMENTS: 1090-012002 (922B)
CURRENT APPLICATION NUMBER: US/11/176,830
CURRENT FILING DATE: 2005-07-06
PRIOR PILING DATE: 2003-09-08
PRIOR PILING DATE: 2003-09-08
PRIOR FILING DATE: 2003-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: SCF: 63rd, 102nd, 110th, 115th, 116th, 119th, 126th, 129th, ; OTHER INFORMATION: 158th, 199th, 205th, 207th or 245th Phe is replaced by Val. US-10-519-390-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
  121 KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                  DKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSSKDLKKSFKSPEPRLFTPEEFFRIFN 145
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                                                                                                                                        177 KPFMLPPVAASSLRNDSSSSNRK 199
                                                                                                        181 KPFMLPPVAASSLRNDSSSSNSK 203
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Sequence 529, Application US/11176830

Sequence 529, Application US/11176830

Publication No. US20060020116A1

GENERAL INFORMATION:

APPLICANT: Gartier, Rene

APPLICANT: Gartier, Rene

APPLICANT: Drittanti, Lila

APPLICANT: Drittante

TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding N.

TITLE OF INVENTION: Acid Molecules and Related Applications

TITLE OF INVENTION: Acid Molecules and Related Applications

TITLE OF INVENTION NUMBER: US/11/176,830

CURRENT FILING DATE: 2003-09-08

PRIOR FILING DATE: 2003-03-21

PRIOR APPLICATION NUMBER: 60/457,135

PRIOR APPLICATION NUMBER: 60/457,135

PRIOR APPLICATION NUMBER: 60/409,898

PRIOR APPLICATION NUMBER: 60/409,898
                                                                                                                                                                                                                                                                                                                                                                                  86 DKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSSKDLKKSFKSPEPRLFTPEEFFRIFN 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 RSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVTKPFMLPPVAASSLRNDSSSSNSK 203
                                                                                                                                                                                                                                26 EGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPGMDVLPSHCWISEMVVQLSDSLTDLL
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                                                                     Length 248;
                                                                                                                                                  1; Indels
                                                                 Query Match

84.4%; Score 895; DB 7;
Best Local Similarity 98.9%; Pred. No. 9.9e-74;
Matches 176; Conservative 1; Mismatches 1;
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Publication No. US20060020116A1
GENERAL INFORMATION:
APPLICANT: Gantier, Rene
APPLICANT: Guyon, Thierry
APPLICANT: Drittanti, Lila
APPLICANT: Vega, Manuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CORGANISM: Homo sapiens
US-11-176-830-529
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US-11-176-830-536
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US-11-176-830-529
US-11-176-830-519
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Sequence 519, Application US/20060020116A1

Sequence 519, Application No. US20060020116A1

GENERAL INFORMATION:
APPLICANT: Gantier, Rene
APPLICANT: Usqu, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu TITLE OF INVENTION WUMBER: US/21/176,830

CURRENT APPLICATION NUMBER: 60/457,135

PRIOR PILING DATE: 2003-09-08

PRIOR FILING DATE: 2003-09-09

NUMBER OF SEQ ID NOS: 1306

SOFTWARE: FESTESEQ for Windows Version 4.0

SEQ ID NO 519

LENGTH: 248

HUMBER OF SEQ ID NO 519

LENGTH: 248

HUMBER OF SEQ ID NO 519
                                                                                                                              Sequence 537, Application US/11176830

### Publication No. US2006020116A1

GENERAL INFORMATION:

APPLICANT: Gantier, Rene

APPLICANT: Gantier, Lila

APPLICANT: Drittanti, Lila

APPLICANTON NUMBER: 10/658, 834

FRIOR APPLICATION NUMBER: 60/457,135

PRIOR PELING DATE: 2003-09-08

PRIOR PELING DATE: 2003-09-09

PRIOR PELING DATE: 2003-09-09

PRIOR PELING DATE: 2002-09-09

NUMBER OF SEQ ID NOS: 1306

SOFTWARE: FESTESEQ for Windows Version 4.0

SEQ ID NO 537

LENGTH: 248

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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-11-176-830-519
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84.3%; Score 894; DB 7;
Best Local Similarity 98.9%; Pred. No. 1.2e-73;
Matches 176; Conservative 1; Mismatches 1;
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Job time : 9.02204 secs
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CORGANISM: Homo sapiens
US-11-176-830-499
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US-11-176-830-538

i Sequence 538, Application US/11176830

i Publication No. US20060020116A1

GENERAL INFORMATION:

APPLICANT: Garder

APPLICANT: Oritanti, Lila

APPLICANT: Vega, Manuel

TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu

TITLE OF INVENTION: Acid Molecules and Related Applications

CURRENT PILING DATE: 2005-07-06

PRIOR PELING DATE: 2003-09-09

PRIOR APPLICATION NUMBER: 60/457,135

PRIOR APPLICATION NUMBER: 60/457,135

PRIOR APPLICATION NUMBER: 60/457,135

PRIOR APPLICATION NUMBER: 60/467,135

PRIOR APPLICATION NUMBER: 60/457,135

PRIOR APPLICATION NUMBER: 60/409,898

PRIOR APPLICATION NUMBER: 60/409,898

PRIOR FILING DATE: 2002-09-09

NUMBER OF SEQ ID NOS: 1306

SEQ ID NO 538

LENGTH: 248
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TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding N TITLE OF INVENTION: Acid Molecules and Related Applications
FILE REPERENCE: 17109-012002 (922B)
CURRENT APPLICATION NUMBER: US/11/176,830
CURRENT FILING DATE: 2005-07-06
PRIOR PRILING DATE: 2005-07-08
PRIOR PLING DATE: 2003-09-08
PRIOR PLING DATE: 2003-09-08
PRIOR PLING DATE: 2003-09-09
PRIOR PLING DATE: 2003-09-09
NUMBER OF SEQ ID NOS: 1306
SEQ ID NOS: 1306
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US-11-176-830-536
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US-11-176-830-538
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New naturally-occurring polypeptide stem cell factor analogues - have haematopoietic biological activity of stem cell factor and are used to treat e.g. leukopenia, AIDS, nerve damage and infertility.
                                                                                                                                                                                                                           Stem cell factor; SCF; leukopenia; AIDS; haematopoiesis.
                                                                                                                                                                                                               Human Stem Cell Factor from HT1080 fibrosarcoma line
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ADW93106
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90US-00537198.
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Zsebo KM, Suggs SV,
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N-PSDB; AAQ11542.
(AMGE-) AMGEN
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11-JUN-1990;
24-AUG-1990;
28-SEP-1990;
01-OCT-1990;
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Peptide
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747.047 Million cell updates/sec
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Biocceleration Ltd
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Match
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Post-processing:

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Minimum DB Maximum DB

Score

Result

Title: Perfect score:

Sequence:

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OM protein

Run on:

Scoring table:

Searched:

The SCF has the ability to stimulate growth of primitive progenitors including early hematopoietic progenitor cells and non- hematopoietic

Disclosure; Fig 42; 127pp; English

Human Human Human Human Human

ADP99319 ADU50661 ADU50649 ADW93094

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(first entry)
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Astches 273; Conservative
                            Lyman S;
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                                                              WPI; 1992-041558/05.
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                            Williams DE,
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15-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                           KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSOCVVSSTLSPEKOSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                              KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
stem cells such as neural stem cells and primordial germ stem cells. The product may be used in a pharmaceutical compsn. for treating, in a mammal, leukopenia, thrombocytopenia, anaemia, AIDS, neoplasia, nerve damage, infertility and intestinal damage. See also AARI1708, AAQ11509-011543
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                                                                                                                                                                                                                                              KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
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                                                                                                                                                                                                                               1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                   MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                                                                                                             Gaps
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0
                                                                                                                                                       Length 273;
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                                                                                                                                                                              133;
0; Indels
                                                                                                                                                     100.0%; Score 1397; DB 2;
100.0%; Pred. No. 2.2e-133;
ive 0; Mismatches 0;
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1. .25
/label= signal
26. .210
/label= extracellular
/note= "claimed polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= transmembrane
238. .273
/label= intracellular
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90US-00565840.
90US-00574152.
90US-00586073.
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                                                                                                                                                                    Best Local Similarity 100.
Matches 273; Conservative
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30-APR-1992 (first en
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                                                                                                                     Sequence 273 AA;
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28-AUG-1990;
21-SEP-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JUN-1990;
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                                                                                                                                                       Query Match
Best Local S
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This human MGF has a mature extracellular region of 185 amino acids. There is a second form of hMGF (see AAQ20844) resulting from an additional use an explicing event which deletes an exon encoding an additional 28 amino acids beginning at amino acid 148 of the mature protein. MGF is the ligand for the protein receptor expression product of the c-kit proto-oncogene. MGF can be used to augment the activity of other cytokines. It can influence early lymphoid or myeloid development. See also AAQ20842-3 and AAQ22204-7. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKOFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 KPFWLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAWALPALFSLIIGFAFGALYWKKR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                   to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKKTQTWILICIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLFKDYMITLKYVPG
New isolated DNA encoding human mast cell growth factor - useful in stimulating proliferation of haematopoietic cells with growth factor, treat haemolytic and hypo;proliferative anaemias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 1397; DB 2; Length 273; 100.0%; Pred. No. 2.2e-133; ive 0; Mismatches 0; Indels 0;
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    .25
    /label= sig_peptide
    .248
    /label= mat_SCF

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                                                                                                                                     Claim 10; Fig 4; 59pp; English.
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AAR83978 is a human stem cell factor (SCF) derived from the HT1080
fibrosarcoma cell line. Non-naturally occuring SCF and C-terminally
curricated polypetides, having amino acid sequences sufficiently
duplicative of naturally ocurring SCF, stimulate growth of primitive
progenitors such as haematopoietic progenitor cells, neural stem cells
and primordial germ stem cells. The peptides can be used in a composition
for treating leucopenia, anaemia or thrombocytopenia, for enhancing
engraftment of bone marrow during transplantation or for bone marrow
convery after chemcherapy or radiation-induced bone marrow aplasia, nerve
damage, infertility, intestinal damage or myeloproliferative disorders.
Antibodies may be raised against the peptides for use in detection or
myelosupplastiantion of SCF in serum. SCF may be useful for the treament of
AIDS and severe combined immunodeficiency (SCID) states alone or in
combination with other factors such as IL-7. (Updated on 25-MAR-2003 to
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                                                                                                                                                                                                        Martin FH;
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                                                                                                                                                                                                                                                                                                                                                 9; Fig 42; 127pp; English.
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                                                                        89US-00422383.
90US-00537198.
90US-00573616.
90WO-US005548.
90US-00589701.
                                               95EP-00105391
                                                                                                                                                                                                        Zsebo KM, Suggs SV,
                                                                                                                                                                                                                                      WPI; 1995-346090/45
                                                                                                                                                                         (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                     N-PSDB; AAT04890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 273 AA;
                                                                                          11-JUN-1990;
24-AUG-1990;
28-SEP-1990;
                                              04-OCT-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stem cell factor analogue N10D or N10D/N11D - useful to treat pigmentation disorder, AIDS, nerve damage, infertility, intestinal damage or haematopoietic disorder.
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                                                                                                                                                                                                                    1. .25
/label= leader sequence
/label= leader sequence
/note= "mature full length stem cell factor protein"
                                                                                Stem cell factor; SCF; mast cell growth factor; MCGF; Steel factor; SLF; analogue; treatment; haematopoietic factor; progenitor cell; pigmentation disorder; haematopoietic disorder.
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                                                   Human recombinant stem cell factor protein.
                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Fig 1; 42pp; English.
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                                                                                                                                                                Homo sapiens
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                   28-APR-1998
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(AMGE-) AMGEN INC.
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   Sequence 273 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-NOV-1992;
21-DEC-1993;
24-MAY-1995;
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01-OCT-1990;
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                                                                                                                                                                                                                                                                                                                                                                   A method has Deen developed or maxing negative cuts subtract to administration to a subject. The method comprises: (a) obtaining the dematopoietic progenitor cells from a donor; and (b) expanding the cells by adding to the cells a haematopoietically effective dose of a polypeptide product having at least part of the primary structural confirmation and one or more of the biological properties of naturally confirmation and one or more of the biological properties of naturally confirmation and one or more of the biological properties of naturally confirmation are capable of maturing to erythroid, megakaryocyte, granulocyte, lymphocyte and macrophage cells. SCF results in absolute increases in hemantopoietic cells of both myeloid and lymphoid lineages. SCF is useful for treating haematopoietic disorders. The method is useful for expanding early haematopoietic progenitors in syngeneic, allogeneic contact of gene therapy based on transfecting haematopoietic stem cells. SCF is also useful for combating the myelosuppressive effects of anti-HIV drugs such as AZT and for enhancing haematopoietic recovery after acute blood loss and as a boost to the immune system for fighting compalsia (cancer). The present sequence represents a specifically compalsia (cancer). The present invention
method has been developed of making haematopoietic cells suitable for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Production of hematopoietic cells suitable for administration to a subject using progenitor cells and expanding the cells using stem cell
                                                                                                                                                                                                                             forming;
                                                                                                                                                                                                                            Stem cell factor; SCF; haematopoietic progenitor cell; blood forming primitive progenitor cell; haematopoietic disorder; syngeneic; allogeneic; arologous bone marrow transplant; gene therapy; transfection; haematopoietic stem cell; acute blood loss; neoplasia;
                                                                                                                                                                                                    Human SCF protein isolated from the HT1080 fibrosarcoma cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Martin FH;
                                                     241 QPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
                                      QPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
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                                                                                                                            AAY53284 standard; protein; 273
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90US-00537198.
90US-00573616.
90WO-US005548.
90US-00589701.
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N-PSDB; AAA13714.
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                                                                                                                                                                                                                                                                                                       Homo sapiens.
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04-OCT-1990;
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                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                                 61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                  121 KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKOFVVASETSOCVVSSTLSPEKOSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALFSLIIGFAFGALYWKKR 240
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                                                                                                                                         1 MKKTQTWILITCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDXMITLKXVPG
                                                                                                                                                                                                                       MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
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  Length 273;
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100.0%; Score 1397; DB 3;
100.0%; Pred. No. 2.2e-133;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human SCF protein sequence SEQ ID NO:61
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90US-00537198.
90US-00573616.
90US-00589701.
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93US-00172329.
95US-00449653.
98US-00005893.
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                                 Best Local Similarity 100.
Matches 273; Conservative
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vitro, comprising exposing (II) that expresses a stem cell factor (SCF) receptor to a biologically active SCF, its analogue or fragment, which induces cell proliferation, and introducing (I) to (II) in vitro. Exposure of SCF to (II) results in increased uptake of (I) into the cell. The method is useful for enhancing the efficiency of the transfer of a polynucleotide into a terget mammalian cell in vitro. The method is useful in gene therapy techniques. Addition to Addition of the present AAB99390 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                   MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                           Query Match 100.0%; Score 1397; DB 4; Length 273; Best Local Similarity 100.0%; Pred. No. 2.2e-133; Matches 273; Conservative 0; Mismatches 0; Indels 0
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90US-00537198.
90US-00573616.
90US-0058701.
92US-00982255.
93US-00172322.
95US-00449653.
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11-JUN-1990;
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01-OCT-1990;
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12-JAN-1998;
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                                                Enhancing efficiency of transfer of polynucleotide into a target mammalian cell in vitro, involves exposing cell that expresses a stem cell factor receptor to stem cell factor, and introducing polynucleotide into cell in vitro.
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anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; stem cell factor; SCF; early haematopoietic progenitor cell;
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100.0%; Score 1397; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.2e-133;
Matches 273; Conservative 0; Mismatches 0;
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/label= Signal_peptide
26. .273
/label= Mature_SCF
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                                                                                                                      Example 3; Fig 16; 210pp; English.
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                                                                                                                                                                                                                                                                                                                       Sequence 273 AA;
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The present invention provides the protein and coding sequences of mammalian stem cell factors (SCFs). These are capable of stimulating the growth of early haematopoietic progenitor cells, neural stem cells and primordial germ stem cells. The sequences are useful in the treatment of leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal naemoglobinuria, malaria, pigmentation disorders, neurological and intestinal damage, infertility, AIDS and severe combined immunodeficiency (SCID). The present sequence is an SCF described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated non-human mammalian stem cell factor polypeptide stimulating growth of early hematopoietic progenitor cells, useful for treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar,
                                                                          Human; rat; mammal; stem cell factor; SCF; cell growth stimulation; gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia; neurological damage; intestinal damage; infertility; AIDS; SCID; severe combined immunodeficiency.
                                         Human stem cell factor SEQ ID NO: 49.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Fig 16; 209pp; English.
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90US-00537198.
90US-00573616.
90US-00589701.
92US-00982255.
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13-JUL-2001 (first entry)
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Matches 273; Conservative
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                                                                                                                                                                                         Ното варіелв.
                                                                                                                                                                                                                                                                                                                  09-NOV-1994;
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01-OCT-1990;
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                                                                                                                                                                                                                                                                                                                                                                                 11-JUN-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence representing human SCF (stem cell factor) protein is isolated from the HT1080 fibrosarcoma cell line. The present invention call sequence from the HT1080 fibrosarcoma cell line. The present invention cells and the collaboration cells from the HT1080 fibrosarcoma cells. Adu02453, Adu02458, Adu02461, and the collaboration cells including early haematopoietic progenitor cells. The invention also describes SCF peptides (Adu02462-Adu02481) and the oligonucleotides.

(AASO4081-AASO4117) used in the isolation of human and rat SCF sequences. The polynucleotide encoding SCF is useful for producing SCF and useful in the isolation of human, and rat SCF sequences. The polynucleotide encoding SCF is useful for producing SCF and useful in the isolation, as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia, congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis, disseminated fungus disease, Pulminating septicemia, malaria, vitamin B12 and folic acid deficiency, pyridoxine deficiency, and hypopigmentation constitution as piebaldism and vitiligo
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                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids encoding stem cell factor useful for treating disorders involving blood cells, e.g. leukemia, splenomegaly, Hodgkin's disease, Kala azar, anemia and septicemia.
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                                                                                                                                                                                                                                                                            Suggs SV, Martin FH;
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                                                           90US-00537198.
90US-00573616.
90US-00589701.
93US-00172329.
                                           89US-00422383
95US-00482918
                                                                                                                                                                                                                                                                            Bosselman RA,
                                                                                                                                                                                     BOSSELMAN R A.
SUGGS S V.
                                                                                                                                                                                                                                                                                                                    2001-298941/31.
                                                                                                                                                                                       (BOSS/) BOSSELMAN R
(SUGG/) SUGGS S V.
(MART/) MARTIN F H.
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                                                                                                                                                                      ZSEB/) ZSEBO
                                                                              24-AUG-1990;
01-OCT-1990;
21-DEC-1993;
    07-JUN-1995;
                                           16-0CT-1989
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Matches

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Martin FH;

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                                             Gaps
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Length 273;
                                          Indels
100.0%; Score 1397; DB 4;
100.0%; Pred. No. 2.2e-133;
tive 0; Mismatches 0;
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AAB96942 standard; protein; 273

AAB96942

AAB96942

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181 KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated non-human mammalian stem cell factor polypeptide stimulating growth of early hematopoietic progenitor cells, useful for treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar, sarcoidosis.
KOLKKSFKSPEPRLFTPERFFRIFNRSIDAPKDFVVASETSDCVVSSTLSPEKDSRVSVT
                    121 KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAPKOFVVASETSOCVVSSTLSPEKDSRVSVT
                                                                  KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
                                                                                                                                                                                                                                                                                                                                                                                                     Human; rat; mammal; stem cell factor; SCF; cell growth stimulation; gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia; neurological damage; intestinal damage; infertility; AIDS; SCID;
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                                                                                                                                  Suggs SV, Martin
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90US-00537198.
90US-00573616.
90US-00589701.
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24-AUG-1990;
01-OCT-1990;
25-NOV-1992;
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121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                     Human; rat; mammal; stem cell factor; SCP; cell growth stimulation; gene therapy; haematopoletic disorder; aplastic anaemia; leukaemia; neurological damage; intestinal damage; infertility; AIDS; SCID; severe combined immunodeficiency.
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                                                                                                                                                                                                                                                                                                                                                                  /label= mature_stem_cell_factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Martin FH;

    .25
    /label= signal_peptide
    .273

                                                                                                                                    stem cell factor SEQ ID NO: 48
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                               AAB96941 standard; protein; 273
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N-PSDB; AAF89102.
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                                                                                                                                                                                                                                                               Homo sapiens
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01-OCT-1990;
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11-JUN-1990;
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                                                                AAB96941;
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                                                                                                                                    Human
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8 셤 ઠ 셤

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The present sequence representing human SCF (stem cell factor) protein is isolated from the HT1080 fibrosarcoma cell line. The present invention crlates to novel stem cell factors (AAB73561-AAB735571-AAB73556) and the polynucleotides encoding them. SCF stimulate primitive progenitor cells including early haematopoletic progenitor cells. The invention also describes SCF peptides (AAB73578-AAB73597) and the oligonucleotides (AAB73359) and the oligonucleotides (AAB73359) and the oligonucleotides (AAB73859) used in the isolation of human and rat SCF sequences. The polynucleotide encoding SCF is useful for producing SCF and useful in gene therapy. It is useful for treating disorders involving blood calls such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple myeloma, Hoddkin's disease, lymphom, Gaucher's disease, anaemia, congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis, disseminated fungus disease, Pulminating septicaemia, malaria, vitamin 312 and folic acid deficiency, pyridoxine deficiency, and hypopigmentation disorders such as piebaldism and vitiligo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKKTQTWILITCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLFKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 MDVLPSHCWISEMVVQLSDSLTDLLDKRSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
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                                                                                                                                                                                                                                                                                                             Length 273;
                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human SCF protein isolated from the HT1080 fibrosarcoma
                                                                                                                                                                                                                                                                                                           100.0%; Score 1397; DB 4;
100.0%; Pred. No. 2.2e-133;
ive 0; Mismatches 0;
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/label= Signal_peptide
Claim 7; Fig 42A-42C; 166pp; English.
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/label= Mature_SCF
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                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 273; Conservative
                                                                                                                                                                                                                                                                                 Sequence 273 AA;
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                                                                                              1 MKKTQTWILTCIYLQLLLENPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                           MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
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                                                                             MKKTQTW1LTC1YLQLLLFNPLVKTEG1CRNRVTNNVKDVTKLVANLPKDYM1TLKYVPG
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blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
anaemia; Kala azar; septicaemia; malaria; hypopigmentation disorder;
                                               Gaps
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                Length 273;
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              100.0%; Score 1397; DB 4;
100.0%; Pred. No. 2.2e-133;
cive 0; Mismatches 0;
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/label= Signal_peptide
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/label= Mature_SCF
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90US-00537198.
90US-00573616.
90US-00589701.
91US-00684535.
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                                               Matches 273; Conservative
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N-PSDB; AAH23901.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HT1080 fibrosarcoma
              Query Match
Best Local Similarity
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The present sequence represents human stem cell factor (SCF). The cDNA encoding this sequence is isolated from the HT1080 fibrosarcoma cell line. The sequence is described in an invention relating to novel stem cell factors, the polynucleotides encoding them and methods for producing the stem cell factors. The methods involve increasing the number of early haematopoietic progenitor cells in human peripheral blood by administering a haematopoietically effective human stem cell factor polypoptide. The methods are useful for the treatment of blood disorders, including myelofibrosis, myelosclerosis, osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease, ilymphoma, Gaucher's disease, Niemann-Pick disease, refractory anaemia, malain, vitamin B12 and folic acid deficiency, hypopigmentation disorders i.e. piebaldism and viral induced disorders, including AIDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Increasing the number of early hematopoietic progenitor cells in the peripheral blood useful for the treatment of blood disorders including Hodgkin's disease comprises the administration of human stem cell factor.
Human, stem cell factor; SCF; haematopoietic progenitor cell; AIDS; blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency; hypopigmentation disorder; viral disorder; HT1080 fibrosarcoma.
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100.0%; Pred. No. 2.2e-133;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                            /note= "Encoded by ATT"
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                                                                                                                                                     1. .25
/label= Signal_peptide
                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                              26. .273
/label= Mature_SCF
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90US-00589701.
91US-00684535.
92US-00982255.
93US-00172329.
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BOSSELMAN R A.
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                                                                                                                                                                                                                                                                               Misc-difference 258
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(SUGG/) SUGGS S V.
(MART/) MARTIN F H.
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Best Local Similarity
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01-OCT-1990;
10-APR-1991;
25-NOV-1992;
21-DEC-1993;
                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence representing human SCF (stem cell factor) protein is isolated from the HT1080 fibrosarcoma cell line. The present invention relates to novel stem cell factors (AAM02767, AAM02770-AAM02775, AAM02779) and the polymuclectides encoding them. SCF stimulate primitive progenitor cells including early haematopoietic progenitor cells. The invention also describes SCF peptides (AAM02777-AAM02794) and the olymuclectides (AAM02777-AAM02795) and the care SCF sequences. The polymuclectide encoding SCF is useful for rat SCF sequences (AAS04182-AAS04218) used in the isolation of human and rat SCF sequences (AAS04182-AAS04218) used in the isolation of human and rat SCF sequences (AAS04182-AAS04218) used in the isolation of human and care SCF sequences (AAS04218) used in the isolation of human and rat SCF sequences (AAS04218) used in the isolation of human and carcinoma, acute leukaemia, multiple myelofibrosis, metastatic carcinoma, acute leukaemia, multiple myelofibrosis, alisease, lansemia, congestive splenomegaly, Kala azar, lancolosis, military tuberculosis, disseminated fungus disease, pulminating septicemia, malaria, vitamin B12 and folic acid deficiency, pyridoxine deficiency, and hypopigmentation disorders such as piebaldism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                   , encoding polypeptide product useful for early hematopoietic progenitor cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 1397; DB 4; Length 273; Pred. No. 2.2e-133; 0; Mismatches 0; Indels 0.
                                                                                                                                                                                              Martin FH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPSLITRAVENIQINEEDNBISMLOEKEREFOEV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPSLIRAVENIQINEEDNEISMLOEKEREFOEV 273
                                                                                                                                                                                                                                                                                                                                                                Example 5; Fig 42A-42C; 167pp; English.
                                                                                                                                                                                            Sugga SV,
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                     89US-00422383.
90US-00537198.
90US-00573616.
90US-00589701.
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                                                                                                           92US-00982255
                                                                                                                                                                                              Bosselman RA,
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                                                                                                                                                                                                                                                                                                     Isolated DNA sequence,
                                                                                                                                                                                                                                                                                                                         stimulating growth of
                                                                                                                                                                                                                                    WPI; 2001-281051/29.
N-PSDB; AAS04224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 273; Conserv
                                                                                                                                                  (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 273 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and vitiligo
                                                                                                           25-NOV-1992;
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                                           1-JUN-1990
                                                                                       01-OCT-1990
                                                                 24-AUG-1990
                                                                                                                                                                                              Zsebo KM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU05266
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                                     KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; stem cell factor; SCF protein; leucopaenia; thrombocytopaenia; anaemia; myelosuppression; nerve damage; myeloproliferative disorder; infertility; neoplasia; myelofibrosis; myelogroliferative disorder; metastatic carcinoma; acute leukaemia; multiple myeloma; sarcoidosis; Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease; Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar; bi Guglielmo syndrome; consestive splenomegaly; splenic pancytopaenia; diseaminated fungus disease; Pulminating septicaemia; piebaldism; AIDS; acquired immune deficiency syndrome; malaria; military tuberculosis; pyridoxine deficiency; vitemin B12 deficiency; folic acid deficiency; blamond Blackfan anaemia; hypopigmentation disorder; vitiligo.
                                                                                                                                                              KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT
                                                                                                                                KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel non-naturally-occurring stem cell factor polypeptide, useful streating leucopenia, thrombocytopenia, anemia and for enhancing engraftment of bone marrow during transplantation in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Mature human SCF protein"
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                                                                                                                                                                                                                                                                                                  OPSLIRAVENIQINEEDNEISMLOEKEREFOEV 273
                                                                                                                                                                                                                                                                OPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
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/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE22326 standard; protein; 273 AA
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(BOSS/) BOSSELMAN R A.
(SUGG/) SUGGS S V.
(MART/) MARTIN F H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human SCF protein #2.
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N-PSDB; AAD35477
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consering and for enhancing bone marrow recovery in treatment of radiation, engraftment of bone marrow during transplantation in mammals and chemical or chemortherapeutic induced bone marrow aplasia or myelosuppression. They are also useful for treating acquired immune deficiency in a human, nerve damage, neoplasia, infertility, myeloproliferative disorder, intestinal camage, neoplasia, infertility, myeloproliferative disorder, intestinal carrive polymer polypeptide adduct, for enhancing transfection of early cative polymer polypeptide adduct, for enhancing transfection of early cative polymer polypeptide adduct, for enhancing transfection of early cative polymer polypeptide adduct, for enhancing transfection of early cative polymer polypeptide adduct, for enhancing myelofibrosis, myelosclerosis, osteopetrosis, metastatic carcinoma, acute leukaemia, myeloma, costeopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma, Hoddkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease, Letterer-Siwe disease, refractory erythroblastic anaemia, pridapielmo sylancome, congestive splenomegaly, Kala azar, sarcoidosis, primary splenic pancycopaemia, diseaminated fungue disease, malaria, military tuberculosis, Pulminating septicaemia, pyridoxine deficiency, vitamin B12 and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation disorders such as piebaldism, AlDS (acquired immune deficiency syndrome) can disorders such as piebaldism, AlDS (acquired immune deficiency syndrome)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
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Best Local Similarity 100.
Matches 273; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 273 AA;
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1164.223 Million cell updates/sec Run on:

US-10-620-642-61 1397 Title: Perfect score:

1 MKKTQTWILITCIYLQLLLLFN.....NEEDNEISMLQEKEREFQEV 273 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	mast cell growth f	mast cell growth f	В	병	_	Ä	_	_	_	stem cell factor p	stem cell factor l	Н	_	_		flagellar hook-len	hypothetical prote	probable advanced	conserved hypothet	probable membrane	hypothetical prote	hypothetical prote	u	hypothetical prote			hypothetical prote		citrate (pro-3S)-1
SUMMARIES	ΩI	359	B61190	146575	847571	146929	865801	A37934	S58313	B35974	JN0637	S70366	S70367	S29052	B35971	A35971	H97165	T16086	T09062	F90595	S61667	F82909	T25944	B86461	T27886	T19295	B69616	T19850	I53340	G86773
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ALIGNMENTS

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		factor precursor
		factor
		growth
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RESULT 1
A35974

mate cell growth factor precursor - human
N;Alternate names: kt ligand; stem cell factor
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 09-Jul-2004
C;Accession: A35974; A61190
R;Martin, F.H.; Suggs, S.V.; Langley, K.E.; Lu, H.S.; Ting, J.; Okino, K.H.; Morris, C.F.
S, JOS-211, 1990
A;Title: Primary structure and functional expression of rat and human stem cell factor L
A;Reference number: A35974; MUID:91004219; PMID:2208279
A;Accession: A35974

A;Molecule type: mRNA
A;Residues: 1-273 cMRNA;Residues: 1-273 cMRNA;Residues: 1-273 cMRNA;Crose-references: UNIPROT:P21583; UNIPARC:UPI000002D482; GB:M59964; NID:g337933; PIDN
B;Anderson, D.M.; Williams, D.E.; Tushinski, R.; Gimpel, S.; Eisenman, J.; Cannizzaro, J.
Cell Growth Differ. 2, 373-378, 1991
Cell Growth Differ. 2, 373-378, 1991
A;Title: AAlternate splicing of mRNAs encoding human mast cell growth factor and localiza A;Reference number: A61190; MUID:92172791; PMID:1724381

A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: mNNAA,ARseidues: 1-273 <AND>
A;Residues: 1-273 <AND>
A;Residues: 1-273 <AND>

A,Gene: GDB:MGF A,Cross-references: GDB:128026; OMIM:184745

A; Map position: 12q22-12q22

C;Superfamily: mouse mast cell growth factor
C;Superfamily: mouse mast cell growth factor
C;Keywords: alternative splicing; extracellular protein; glycoprotein; transmembrane pro
C;Keywords: alternative splicing; extracellular protein; glycoprotein; transmembrane profits
F;126-273/Product: mast cell growth factor #status predicted «MCS»
F;26-139/Product: (or 26-190) mast cell growth factor, soluble form #status predicted «IMM»
F;215-237/Domain: transmembrane #status predicted «IMM»
F;90,97,118,145,195/Binding site: carbohydrate (Asn) (covalent) #status predicted

ö Gaps ö Query Match 100.0%; Score 1397; DB 2; Length 273; Best Local Similarity 100.0%; Pred. No. 2e-101; Matches 273; Conservative 0; Mismatches 0; Indels 0.

9 1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG g Š

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9 9

Gaps

1;

179

239

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stem cell factor, longer isoform - bovine
c;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C;Accession: 847571
R;Zhou, J.H.; Hikono, H.; Ohtaki, M.; Kubota, T.; Sakurai, M.
R;Zhou, J.H.; Hikono, H.; Ohtaki, M.; Kubota, T.; Sakurai, M.
R;Zhou, J.H.; Hikono, H.; Ohtaki, M.; Kubota, T.; Sakurai, M.
R;Zhou, J.H.; Hikono, H.; Ohtaki, M.; Kubota, T.; Sakurai, M.
R;Zhitle: Cloning and characterization of coNAs encoding two normal isoforms of bovine st
A;Reference number: 847571; MUID:94339176; PMID:7520283
A;Resedues preliminary
A;Molecule type: mRNA
A;Residues: 1-274 < CADA
A;Residues: 1-274 < CADA
A;Cross-references: UNIPROT:Q28132; UNIPARC:UPI0000135639; EMBL:D28934; NID:g538520; PID)
C;Superfamily: mouse mast cell growth factor
                        A;Molecule type: mRNA
XResidues 1.274 «ZHA»
A;Cross-references: UNIRROT:Q29030; UNIPARC:UPI0000135640; GB:L07786; NID:g164420; PIDN:
C;Superfamily: mouse mast cell growth factor
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                                                                                                                                                      DB 2; Length 274;
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84.8%; Score 1184.5; DB 2; Length
Best Local Similarity 84.7%; Pred. No. 7.1e-85;
Matches 232; Conservative 20; Mismatches 21; Indels
                                                                                                                                                                                                       Indels
                                                                                                                                                    Query Match 86.1%; Score 1203.5; DB 2; Best Local Similarity 85.8%; Pred. No. 2.4e-86; Matches 235; Conservative 22; Mismatches 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 KQPNLTRTVENIQINEEDNEISMLQEKEREFQEV 274
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                  RESULT 2
Bast cell growth factor, short form precursor - human
NyAlternate names: kit ligand, short form; stem cell factor, short form
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: B61190
R;Adderson, D.M.; Williams
D; Tuthinski, R.; Gimpel, S.; Eisenman, J.; Cannizzaro, I R;Adderson, D.M.; Williams
A;Title: Alternate splicing of mRNAs encoding human mast cell growth factor and localiza
A;Reference number: A61190; MUID:92172791; PMID:1724381
A;Reference number: A61190; MUID:92172791; PMID:1724381
A;Reference number: A61190; MUID:92172791; PMID:1724381
A;Residues: 1-245 AND
A;Residues: 1-245 AND
A;Residues: 1-245 AND
A;Gene: GDB:MGF
A;Gene: GDB:MGF
A;Gene: GDB:MGF
A;Gene: GDB:MGF
A;Gene: GDB:MGF
A;Gene: GDB:MGF
A;Map position: 12q22-12q22
C;Superfamily: mouse mast cell growth factor
C;Genetics: alternative splicing; glycoprotein; transmembrane protein
F;1-25/Domain: signal sequence #status predicted <SIG>F;B7-209/Domain: transmembrane #status predicted
F;90,97,118,145/Binding site: carbohydrate (Asn) (covalent)
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C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 2.7 Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: 146575
R;Zhang, Z.; Anthony, R.V.
R;Zhang, Z.; Anthony, R.V.
A;Title: Porcine stem cell factor/c-kit ligand: its molecular cloning and localization
A;Reference number: 146575; MUID:94146218; PMID:7508758
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                                                     MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                         OBSLTRAVENIOINEEDNEISMLOEKEREFOEV 273
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Gaps

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179

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A;Cross-references: UNIPARC:UP1000017955D; GB:M38511
R;Anderson, D.M.; Lyman, S.D.; Baird, A.; Wignall, J.M.; Bisenman, J.; Rauch, C.; March, Cell 63, 235-243, 1990
A;Title: Molecular cloning of mast cell growth factor, a hematopoietin that is active is A;Reference number: A35977; MUID:91004223; PMID:1698558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Mosidues: 1-27: AAND-
A; Cross-references: UNIPARC: UPI0000028C9B; GB: MS7647; GB: M38436; NID: 9199151; FIDN: AAA3-
R; Copeland, N.G.; Gilbert, D.J.; Cho, B.C.; Donovan, P.J.; Jenkins, N.A.; Cosman, D.; Acell 63, 175-183, 1990
Cell 63, 175-183, 1990
A; Title: Mast cell growth factor maps near the steel locus on mouse chromosome 10 and i
A; Reference number: A35972; MUID: 91004216; PMID: 1698554
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 26-23 < COD>
A; Costanaes: 26-23 < COD>
A; Cross-references: UNIPPRC: UP1000017955E; GB: M59912
B; Zsebo, K.M.; Williams, D.A.; Geissler, B.N.; Broudy, V.C.; Martin, P.H.; Atkins, H.L.,
Cattanach, B.M.; Galli, S.J.; Suggs, S.V.
A; Title: Stem cell factor is encoded at the Sl locus of the mouse and is the ligand for A; Reference number: A35975; MUID: 91004220; PMID: 1698556
A; Accession: A35975.
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A; Mesidues: 1-201 <2258.
A; Mesidues: 1-201 <2258.
A; Cross-references: UNIPARC: UP1000016D02D; GB: M59915; NID: g200935; PIDN: AAA40095.1; PID
R; Zsebo, K.M.; Wypych, J.; McNiece, I.K.; Lu, H.S.; Smith, K.A.; Karkare, S.B.; Sachdev,
R; Langley, K.B.
Cell 63, 195-201, 1990
A; Title: Identification, purification, and biological characterization of hematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPARC:UP1000017955F
R;Brannan, C.I.; Bedell, M.A.; Resnick, J.L.; Eppig, J.J.; Handel, M.A.; Williams, D.E.,
Genes Dev. 6, 1832-1842, 1992
A;Title: Developmental abnormalities in Steell7H mice result from a splicing defect in t
A;Reference number: A44071; MUID:93012940; PMID:1383087
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A;Molecule type: mRNA
A;Residues: 1-206,'S',208-273 <RES>
A;Cross-references: UNIPARC:UPIO00016CA07; EMBL:X68989; NID:g395283; PIDN:CAA48778.1; Pī
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C;Keywords: extracellular protein; glycoprotein; transmembrane protein
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82.8%; Pred. No. 9.8e-83;
ive 19; Mismatches 28; Indels
A;Status: preliminary; not compared with conceptual translation
                                                 A; Molecule type: mRNA
A; Residues: 1-206, 'S', 208-270 <HU2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Molecule type: protein
A, Residues: 27-29, 'R', 31-39 <252>
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Matches 226; Conservative
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S65801
mast cell growth factor - mouse
NyAlternate names: hematopoietic growth factor KL; ligand steel factor; stem cell factor
C;Species: Mus musculus (house mouse)
C;Date: 28 - Oct. 1996 #sequence revision 27-Feb-1997 #text change 09-Jul-2004
C;Accession: S65801; A43751; Ā35976; A35972; A35975; A35975; A35973; I48768
R;Bedell, M.A.; Copeland, N.G.; Jenkins, N.A.
Genetics 142, 927-934, 1996
A;Title: Multiple pathways for Steel regulation suggested by genomic and sequence analys
A;Reference number: S65801; MUD:97002551; PMID:8849898
A;Accession: S65801
A;Residues: 1-273 eBBN
A;Residues: 1-273 eBBN
A;Fitle: Differential expression and processing of two cell associated forms of the kit-
A;Accession: A47751
A;Accession: A47751
A;Accession: A47751
A;Accession: A47751
A;Residues: 1-214, L'L, 216-273 eHUA
A;Residues: 1-224, L'L, 216-273 eHUA
A;Res
                                                                          Gispecies: Canis lupus familiaris (dog)
CjSpecies: Canis lupus familiaris (dog)
CjSpecies: Oal-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
CjAccesion: 146929
CjAcc
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A;Status: preliminary
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                                                                                                                                                                                                                                 mast cell growth factor precursor (version 2) - mouse

N;Alternate names: KL-2 protein
C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1991 #sequence_revision 26-Jul-1991 #text_change 09-Jul-2004
C;Accession: A37934; B43751
C;Accession: A37934; B43751
C;Accession: A37934; B43751
A;Title: Transmembrane form of the kit ligand growth factor is determined by alternative
A;Reference number: A37934; MUID:91160046; PMID:1705866
A;Accession: A37934; MUID:91160046; PMID:1705866
A;Accession: A37934
A;Molecule type: mRNA
A;Residues: 1-245 <FRANA
A;Cross-references: UNIPROT: P20826; UNIPARC:UP1000002B352; GB:M64262
B;Huang, B.J.; Nocka, K.H.; Buck, J.; Besmer, P.
Mol. Biol. Cell 3, 348-326, 1992
A;Title: Differential expression and processing of two cell associated forms of the kit-A;Reference number: A43751; MUID:9233001; PMID:1378327
A;Status: prellminary
A;Molecule type: mRNA
A;Cross-references: UNIPARC:UP10000179560; GB:S04534
A;Cross-references: UNIPARC:UP10000179560; GB:S04534
A;Noce: the authors translated the codon TTG for residue 187 as Trp
C;Superfamily: mouse mast cell growth factor
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: S58313
R;McInnes, C.J.; Logan, M.; Falconer, V.M.; Rawlins, P.; Huntly, J.; Haig, D. submitted to the EMBL Data Library, August 1995
A;Description: Molecular cloning and biological activity of ovine stem cell factor.
A;Reference number: S58313
A;Status: Sfalls
A;Status: preliminary
A;Molecule type: mRNA
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1 MKKTQTWIITCIYLQLLLFNPLVKTKEICGNPVTDNVKDITKLVANLPNDYMITLNYVAG
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                                                                           241 OPSLTRAVENIQINEEDNEISMLQEKEREFQEV
                                                                                                      241 QSSLTRAVENIQINEEDNEISMLQQKEREFQEV
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A;Cross-references: UNIPROT:P79368; UNIPARC:UPI000016C4B5; EMBL:Z50743; NID:g940807; PID.
C;Superfamily: mouse mast cell growth factor
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C;Species: Rattus norvegicus (Norway rat)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 09-Jul-2004

C;Accession: B35974; A39805

R;Martin, F.H.; Suggs, S.V.; Langley, K.E.; Lu, H.S.; Ting, J.; Okino, K.H.; Morris, C.F

C,J.; Patel, A.C.; Fisher, B.F.; Brjavec, H.O.; Herrera, C.J.; Wypych, J.; Sachdev, R

C,J.; 1990

A;Title: Primary structure and functional expression of rat and human stem cell factor D)

A;Reference number: A35974; MUID:91004219; PMID:2208279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: B35974
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-201 «MAR»
A;Cross-references: UNIPROT:P21581; UNIPARC:UPI0000144090; GB:M59966; NID:g206861; PIDN:
B;Lu, H.S.; Clogston, C.L.; Wypych, J.; Fausset, P.R.; Lauren, S.; Mendiaz, E.A.; Zsebo, J. Biol. Chem. 266, 8102-8107, 1991
A;Title: Amino acid sequence and post-translational modification of stem cell factor iso A;Reference number: A39805; MUID:91217037; PMID:1708771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 KOLKKSPKSPRPRLFTPREFFRIFNRSIDAFKDF-VVASETSDCVVSSTLSPEKDSRVSV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 ENVKKSSKSPEPRQFTPEKFPGIFNKSIDAFKDLEIVASTMSECVISSTSSPEKDSRVSV 180
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                                                                                                                                                                                                                       1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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                                                                                               Query Match 63.4%; Score 885.5; DB 2; Best Local Similarity 86.1%; Pred. No. 9e-62; Matches 174; Conservative 15; Mismatches 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 'E',271-190 «LUA»
A;Cross-references: UNIPARC:UF1000014F57C
C;Superfamily: mouse mast cell growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 TKPFMLPPVAASSLRNDSSSSN 201
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Matches 166; Conservative
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A; Molecule type: mRNA
A; Residues: 1-233 <PBT>
A; Cross-references: UNIPARC:UP1000002B34F; EMBL:U43079; NID:g1150877; PIDN:AAC59934.1; E
C; Superfamily: mouse mast cell growth factor
C; Keywords: growth factor; transmembrane protein
F; 1-25/Domain: signal sequence #status predicted <SIG>
F; 26-253/Product: stem cell factor short form #status predicted <MAT>
F; 192-216/Domain: transmembrane #status predicted <TMM>
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C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S29052
R;Lu, H.S.; Clogston, C.L.; Wypych, J.; Parker, V.P.; Lee, T.D.; Swiderek, K.; Baltera J.; Langley, K.B.
Arch. Biochem. Biophys. 298, 150-158, 1992
Arch. Biochem. Biophys. 298, 150-158, 1992
A;Title: Post-translational processing of membrane-associated recombinant human stem cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of avian stem cell far
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                                                                                                                                                          61 MDSLPNHCWLHLMVPEFSRSLANLLQKFVDISDMSDVLSNYSIINNLTRIINDLMACLAF 120
                                                                                                                                                                                                                                                                                    61 MDSLPNHCWLHLMVPEFSRSLHNLLQKFVDISDMSDVLSNYSIINNLTRIINDLMACLAF 120
                                                                                                                                                                                                                                                   RVSVTKPFMLPPVAASSLRND-----SSSSNRKAKNPPGDSSLHWAAMALPALFSLIIG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MDVLPSHCWISEMVVQLSDSLTDLLDKF---SNISEGLSNYSIIDKLVNIVDDLVECVKE 117
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C;Date: 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
C;Date: 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
R;Petitte, J.N.; Kulik, M.J.
Biochim. Biochys. Acta 1307, 149-151, 1996
A;Title: Cloning and characterization of cDNAs encoding two forms of avian sA;Reference number: S70366; MUID:96283808; PMID:8679698
                                                                                                                         NSSKO-LKKSPKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASBTSDCVVSSTL-SPEKDS
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C;Species: Homo sapiens (man)
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             Street cell factor precursor - chicken
C;Species: Gallus gallus (chicken)
C;Species: 24-Peb-1994 #sequence_revision 24-Peb-1994 #text_change 09-Jul-2004
C;Accession: JN0637
R;Zhou, J. H.; Ohtaki, M.; Sakurai, M.
Gene 127, 269-270, 1993
A;Title: Sequence of a cDNA encoding chicken stem cell factor.
A;Reference number: JN0637; MUID:93273244; PMID:7684722
A;Reference number: JN0637
A;Molecule type: mRNA
A;Residues: 1-287 <ZHO>
A;Residues: 1-287 <ZHO>
A;Coperimental source: brain
C;Superfamily: mouse mast cell growth factor
C;Keywords: growth factor, transmembrane protein
F;1-25/Domain: signal sequence #status predicted <AIG>F;26-287/Product: stem cell factor #status predicted <ATM>
F;26-248/Domain: transmembrane predicted <ATM>
F;26-248/Domain: transmembrane predicted <ATM>
F;26-248/Domain: stemsmembrane predicted <ATM>
F;26-248/Domain: grants predicted <ATM>
F;26-248/Domain: 
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Stem cell factor long form precursor - quail

C;Species: Coturnix coturnix (quail)

C;Date: 06-Dec.1996 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000

C;Accession: S70366

R;Petitte, J.N.; Kulik, M.J.

Bjochim. Biophys. Acta 1307, 149-151, 1996

A;Title: Cloning and characterization of cDNAs encoding two forms of avian stem

A;Title: Cloning and characterization of cDNAs encoding two forms of avian stem

A;Reference number: S70366

A;Molecule type: mRNA

A;Residues: 1-287 cPET>

A;Cross-references: UNIPARC:UPI000013563D; EMBL:U43078; NID:gl150875; PIDN:AAC59

C;Superfamily: mouse mast cell growth factor

C;Keywords: growth factor; transmembrane protein

F;1-25-Domain: signal sequence #status predicted <MAT>

F;26-287/Product: stem cell factor long form #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 MDSLPNHCWLHLMVPEFSRSLHNLLQKFSDISDMSDVLSNYSIINNLTRIINDLMACLAF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSSKD-LKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTL-SPEKDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.3%; Score 703; DB 2; Length 287; 51.9%; Pred. No. 2.3e-47; ive 50; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 51.9
Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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A;Reference number: S29052; MUID:92398336; PMID:1381905
A;Accession: S29052
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A;Accession: Drotcain
A;Residues: 1-13;14-30;31-46;47-59;60-86;87-95;96-107;108-124 <LUH>
A;Residues: L-13;14-30;31-46;47-59;60-86;87-95;96-107;108-124 <LUH>
CSCOSSE-TEFERENCES: UNIPROT:QTM4N8; UNIPARC:UPI0000179563; UNIPARC:UPI0000179564; UNIPARC;Superfamily: mouse mast cell growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mast cell growth factor - mouse (fragment)
mast cell growth factor - mouse (fragment)
c;Species: Mus musculus (house mouse)
C;Species: Musculus (house mouse)
C;Species: Musculus (house mouse)
C;Accession: A35971
K;Williams, D.B.; Eisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park, R;Williams, D.B.; Eisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park, Cell 63, 167-174, 1990
A;Title: Identification of a ligand for the c-kit proto-oncogene.
A;Reference number: A35971; MUID:91004215; PMID:1698553
A,Accession: A35971
A;Scatus: preliminary
A;Residues: 1-49 <MIL>
A;Residues: 1-49 <MIL>
A;Cross-references: UNIPROT:P20826; UNIPARC:UP10000179561
C;Superfamily: mouse mast cell growth factor
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mast cell growth factor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Accession: B35971
R;Williams, D.E.; Eisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park, R;Williams, D.E.; Eisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park, A;Williams, D.E.; Eisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park, A;Wille: Identification of a ligand for the c-kit proto-oncogene.
A;Reference number: A35971; MUID:91004215; PMID:1698553
A;Accession: B35971
A;Accession: B35971
A;Accession: B35971
A;Residues: 1-51 kWIL>
A;Residues: 1-51 kWIL>
A;Residues: 1-51 kWIL>
C;Superfamily: mouse mast cell growth factor
C;Superfamily: mouse mast cell growth factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                     26 EGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPGMDVLPSHCWISEMVVQLSDSLTDLL 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 DKFSNISEGLSNYSII------DDLVECVKENSSKDLKKSFKSPEPRLFTPEEFFRIFN 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                       0; Indels 41;
                                                                                                                                                                                                                                                                                               Query Match 41.3%; Score 576.5; DB 2; Length 124; Best Local Similarity 75.2%; Pred. No. 5.4e-38; Matches 124; Conservative 0; Mismatches 0; Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
12.6%; Score 175.5; DB 2; Length 51;
Best Local Similarity 72.3%; Pred. No. 2.7e-07;
Matches 34; Conservative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.3%; Score 172.5; DB 2; Length 49; 73.5%; Pred. No. 4.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 ICRNRVTNNVKDVTKLVANLPKDYMITLKYVPGMDVLPSHCWISEMV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSI----DFVVASETSDCVVSSTLSPEKDSRVSVTKPFMLPPVAA 124
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Best Local Similarity
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B35971
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Search completed: February 22, 2006, 18:20:27 Job time: 23.562 secs

OM protein - protein search, using sw model

Pebruary 22, 2006, 18:05:51 ; Search time 140.636 Seconds
 (without alignments)
 1369.555 Million cell updates/sec Run on:

US-10-620-642-61 1397 1 MKKTQTWILTCIYLQLLLFN......NBEDNBISMLQBKBRBFQEV 273 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 seqs, 705528306 residues Searched:

2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

SUMMARIES

	Description	homo sapien	papio cynoc		_	_	9 capra hircu		_	_	homo sapien	rattus norv	mus musculu	3 ovis aries	rattus norv	-	mns musculu					mns musculu		ambystoma m	xenopus lae	/ xenopus lae	xenopus lae	5 brachydanio		_		plasmodium
	Descr	P21583	Q865z4	Q95md2	P79169	029030	Q95m1	028132	006220	Q95n18	Q68dz2	P21581	P20826	P79368	Q54a14	064384	Q78ed8	086419	009108	090314	Q7m4n8	061854	08c9k1	29ygp 2	07zxv0	Q8ayn7	Q6dtw3	056jh6	Q481a5	Q8epm7	0 56jh5	Q8ifm4
SUMMAKIES	ΙD		RIM		45		APHI				Q68DZ2_HUMAN (Q78ED8_MOUSE (Q8C9K1_MOUSE						ETING		RARE	Q8IFM4_PLAF7
	DB	7	~	-	٦	_	-	-	-	-	~	Н	-	-	~	N	~	~	-	-	~	~							~			~
	Query Match Length	273	245	274	274	274	274	274	274	274	238	273	273	267	245	208	208	164	287	287	124	123	160	271	270	270	270	272	234	36	267	1697
df		100.0	87.6	87.3	87.2	86.1	85.0		84.5	84.5	83.8	82.9	85.8	82.8		61.9	61.9	59.8	50.3	50.3	41.3	36.4	34.4	26.8	24.6	21.6	21.4	14.9	11.1	10.4	9.3	9.1
	1	1397	1224	1219.5	1217.5	1203.5	1187.5	1184.5	1180.5	1180.5	1171	1158	1157	1156.5	992	865	865	835	703	702	5.925	509	480	375	343	302	299	207.5	154.5	145	130	127
	Result No.	-	7	٣	4	S	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31

Q8mwp2 plasmodium Q8mwp1 plasmodium Q8mwp1 plasmodium Q8x4d3 plasmodium Q7xem0 plasmodium Q6f1y9 candida gla Q75f78 ashbya goss P54637 dictyosteli Q7xe9 plasmodium Q6ya77 plasmodium Q6ya77 plasmodium Q7yxx2 cryptospori Q97xx6 emericella
08MWP2 FLAFA 08MWP1_PLAFA 08MWP1_PLAFA 042403_PLABE 078EM0_PLAYO 06FLY9_CANGA 07F78_ASHGO PTP3_DICDI 054873_DICDI 054873_DICDI 0778X2_CRYPY 0977XX2_CRYPY 0977XX2_CRYPY
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1711 1713 1716 330 555 1011 373 989 989 990 1231 1666 5542 465
00000000000000000000000000000000000000
127 127 127 116.5 109 108.5 107.5 106.5 106.5 106.5
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8

ALIGNMENTS

RESULT	RESULT 1
1	SCF HUMAN STANDARD; PRT; 273 AA.
AC	16487; Q9UQK7;
TO	l. 18, Creat
L I	01-MAY-1991 (Rel. 18, Last sequence update)
ם ב	10-MAY-2005 (Rel. 47, Last annotation update) wit licend appearance (C-bit licend) (Stom cell feator) (SCR) (Meet
88	דמרנים (פרני)
NB	Name=KITLG; Synonyms=MGF, SCF;
SO	
8	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
8	
3 8	HOMO.
S Z	(1)
RP	NUCLEOTIDE SEQUENCE (ISOFORM 1).
ž	MEDLINE=91004219; PubMed=2208279; DOI=10.1016/0092-8674(90)90301-T;
& :	Martin F.H., Suggs S.V., Langley K.E., Lu H.S., Ting J., Okino K.H.,
\$ 8	Morris C.F., McNiece I.K., Jacobsen F.W., Mendiaz B.F., Birkett N.C.,
8 6	Smith K.A., Johnson M.J., Parker V.P., Flores J.C., Patel A.C.,
5 5	Priblet B.F., Bijavet m.C., Metrera C.O., Wypycum O., Sachaev K.N., Done I h Tealis I was D Tin C -W Comples D I. Vesho K M .
5 5	FOUR O.A., LEGILE I., MELL D., LIN., CUPLES N.L., ESENO N.M., Indiana structure and finations servicesion of rat and himan atom
Į E	rithman actual cure and increasing the captures of the control of
1 G	COLL #21011-211 (1990)
2 2	[2]
2 2	NICLEOTIDE SEQUENCE (ISOFORM 2).
2	PubMed=1724381;
Ą	Anderson D.M., Williams D.E., Tushinski R., Gimpel S., Bisenman J.,
æ	Cannizzaro L.A., Aronson M., Croce C.M., Huebner K., Cosman D.;
RT	"Alternate splicing of mRNAs encoding human mast cell growth factor
RT	and localization of the gene to chromosome 12q22-q24.";
Æ	Cell Growth Differ. 2:373-378(1991).
Z.	[3]
RP	NUCLEOTIDE SEQUENCE (ISOFORM 2).
X	MEDLINE=99160429; Pubmed=10049787; DOI=10.1006/bbrc.1999.0260;
S	Blair H.C., Julian B.A., Cao X., Jordan S.B., Dong S.S.;
RI	"Parathyroid hormone-regulated production of stem cell factor in human
¥ 1	osteoblasts and osteoblast-like cells
2 2	Lalocnem. Biopnys. res. Commun. 255://8-/84(1999).
3 5	ן נין אוינד מיינותים
¥ 6	NOCEDITION SEQUENCE.
ž	nan c., Felig A., Tuan C., Vian B., Vian S., Via
N K	SUBMITTER (OUD-2001) to the EMBL/GenBain/Dubo databases. [4]
2 2	NICHEOTIDE SECTENCE (LARGE SCALE MENA) (ISOBORM 1)
ž	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnds.242603899;
æ	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
æ	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Z	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
\$	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
&	Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
æ	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

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Event=Alternative splicing; Named isoforms=2;
Event=Alternative splicing; Named isoforms=2;
Event=Alternative splicing; Named isoforms=2;
Name=1; Synonyms=SCF248;
IsoId=P21583-1; Sequence=Displayed;
Name=2; Synonyms=SCF248;
IsoId=P21583-2; Sequence=USP 006022;
IsoId=P21583-2; Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MUCLECTIDE SEQUENCE OF 167-248 (ISOFORM 2).

MEDLINE=92360843; PubMed=1379846;

A TOYOCA M., Hinoda Y., Itoh F., Tsujisaki M., Imal K., Yachi A.;

TOYOCA M., Hematol. 15.301-304(1922).

Int. J. Hematol. 55.301-304(1922).

-!- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myceloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins.

-!- SUBCMIT: Homodimer, non-covalently linked (Probable).

-!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci D., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J., Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.B., Schmitz J. Skalska U., Smailus D.B., Schnerch A., Schein J.B., Jones S.J.M., Marra M.A., Schein J.B., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO: GO: 0005886; C:plasma membrane; NAS.
GO: GO: 0005173; F:stem cell factor receptor binding; NAS.
GO: GO: 0008283; P:stem cell factor receptor binding; NAS.
GO: GO: 00030097; P:hemopoiesis; NAS.
GO: GO: 0007165; P:signal transduction; TAS.
InterPro: IPR01235; Cyrokine 4 hlx.
PANTHER: PTHR11574; SCF: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M59964; AAA85450.1; -; mRNA.
EMBL; AT19835; AAD22048.1; -; mRNA.
EMBL; A7400437; AAX022485.1; -; mRNA.
EMBL; BC069733; AA469733.1; -; mRNA.
EMBL; BC069733; AA469733.1; -; mRNA.
EMBL; BC069793; AA469733.1; -; mRNA.
EMBL; BC069797; AA469793.1; -; mRNA.
EMBL; BC074725; AA474725.1; -; mRNA.
EMBL; S42571; AA822846.2; -; mRNA.
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PIR; B61190; B61190.

PDB; IEXZ; X-ray; A/B/C/D=1.273.

Ensembl; ENSG0000049130; Homo sapiens.

MIM; 184745;
                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF02404; SCF; 1.
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1 MKKTQTWILITCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASBTSDCVVSSTLSPEKDSRVSVT
                                                          Kit ligand.

Extracellular (Potential).

Potential.

Cytoplasmic (Potential).

N-linked (GlCNAc. ..) (Potential).

N-linked (GLNAc. ..) (Potential).

N-linked (GLNAc. ..) (Potential).

N-linked (GLNAc. ..) (Potential).

N-linked (GLNAc. ..) (Potential).

By similarity.

By similarity.

Fy similarity.

Fy linker (GlCNAc. ..) (Potential).

Fy linker (GlCNAc. ..) (Potential).

Fy linked (GlCNAc. ..) (Fy linked).

I -> F (IN Ref. 3 and 4; AAK92486).

I -> F (IN Ref. 3 and 4; AAK92486).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Papio.
3D-structure; Alternative splicing; Cell adhesion; Glycoprotein; Growth factor; Signal; Transmembrane.
SIGNAL 1 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1397; DB 1; Length 273; 100.0%; Pred. No. 1.7e-98;
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Kalina T., Storek J.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

SHEMI, N226584; A4072537.1; -; mRNA.

HSSP; P21583; 1EXZ.

SHE, Q86524; 29-161.

SHE, Q8624; 29-161.

SHE, G86301050; Cimembrane; IEA.

G0; G0:001620; F:stem cell factor receptor binding; IEA.

G0; G0:0007155; P:cell adhesion; IEA.

InterPro; IPR003452; SCF.

SEQUENCE 245 AA; 27887 MW; 937B3CAF28D694FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
1-JUNAR-2004 (TrEMBLrel. 26, Last annotation update)
Stem cell factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 QPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
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128 128 K
134 134 L
273 AA; 30899 MW;
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Best Local Similarity 100.0*;
Matches 273; Conservative 0
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Q86524;
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CARBOHYD
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DISULFID
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CONFLICT
CONFLICT
SEQUENCE
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Cell adhesion;
SIGNAL
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A Murray J.D., Bowling A.T.;
The profile of the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

- I- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).

- SUBGELLULAR LOCATION: Type I membrane protein. Also exists as a secreted soluble form (By similarity).

- PTMR A soluble form is produced by proteolytic processing of the extracellular domain (By similarity).

- SIMILARITY: Belongs to the SCF family.
                                                                                 MKKTQTWILICIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                                                                                                                                                             -----KAKNPPGDSSLHWAAMALPAFFSLIIGFAFGALYWKCR
                                                              MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                  MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                                                                                       KOLKKSPKSPEPRLFTPEEFFRI FNRSIDAFKDFVVASBTSDCVVSSTLSPEKDSRVSVT
                                                                                                                                                                                       KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKOFVVASETSDCVVSSTLSPEKG-----
                                                                                                                                                                                                                           KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                      095MD2; 062765; 059MG3; 095MG8; 09N1Y5; 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 47, Last amotation update)
10-MAY-2005 (Rel. 47, Last amotation update)
Kit ligand precursor (C-Kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
Name=KATLG; Synonyms=MGF, SCF;
Bquus caballus (Horse).
Eukaryota; Metacas; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Skin;
states S., Checa-Cortes M.L., Joerg H., Stranzinger G.;
"An equine sequence homologous to stem cell factor (KIT-ligand).";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Terry R.R., Bailey B.F., Cothran B.G.; "Evaluation of MGF as the candidate gene for Appaloosa spotting. Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                       28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1] —
NUCLEOTIDE SEQUENCE OF 4-264.
NUCLEOTIDE SEQUENCE OF 4-264.
Terry R.R., Mickelson J.R., Schmutz S., Cothran E.G., Bailey Teguus caballus mast cell growth factor (MGF).";
"Eguus caballus mast cell growth factor (MGF).";
".hmifred (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                       2; Indels
           87.6%; Score 1224; DB 2;
88.6%; Pred. No. 2.4e-85;
ive 1; Mismatches 2;
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         Query Match
Best Local Similarity 88.6
Matches 242; Conservative
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation - the Ewropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  n; Growth factor; Signal; Transmembrane.
Potential.
Kit ligand.
Extracellular (Potential).
Potential.
Cytoplasmic (Potential).
N-linked (GlCNAc. .) (Potential).
By similarity.
By similarity.
C -> P (in Ref. 2).
Missing (in Ref. 3).
Missing (in Ref. 3).
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28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
11-MAY-2005 (Rel. 47, Last annotation (SCF) (Mast cell growth factor) (MGP).

Name=KITLG; Synonyms=SCF;
12-MAR-KITLG; Synonyms=SCF;
13-MAR-KITLG; Synonyms=SCF;
14-MAR-KITLG; Synonyms=SCF;
15-MAR-KITLG; Synonyms=SCF;
15-MAR-KITLG; Synonyms=SCF;
15-MAR-KITLG; Synonyms=SCF;
15-MAR-KITLG; Synonyms=SCF;
16-MAR-KITLG; Synonyms=SCF;
16-MAR-KITLG;
16-
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                                                                                                                                                                                                                          EMBL; AF401625; AAK94474.1; -; mRNA.
EMBL; AF053498; AAC97076.1; -; mRNA.
EMBL; AF367704; AAK63249.1; -; Genomic_DNA.
EMBL; AF307706; AAK63250.1; -; Genomic_DNA.
EMBL; AF1307706; AAK36716.1; -; Genomic_DNA.
EMBL; AF130770; AAK36716.1; -; Genomic_DNA.
INCEPED: 1PR012251; Cytokine_4_hlx.
INCEPED: IPR012251; Cytokine_4_hlx.
INCEPED: PRN013451; SCF.
PANTHER; PTHR11574; SCF; 1.
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87.2%; Pred. No. 6.2e
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Matches 239; Conservative
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TKPFWLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKK 239
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Pred. No. 1e-83;
                                              ROPSLTRAVENIQINEEDNEISMLOEKEREFOEV
                                                                                                                            274 AA
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PIR; 146575; 146575.
SMR; Q29030; 29-161.
InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR03452; SCF.
PANTHER; PTHR11574; SCF; 1.
PÉan; PP02404; SCF; 1.
Cell adhesion; Glycoprotein; Growth fac
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Best Local Similarity
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SEQUENCE
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TRANSMEM
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029030;
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                                                                                                                                                                                                                                                                                                               This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKOF-VVASETSDCVVSSTLSPEKDSRVSV 179
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                                                                                                                                                               and 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Gaps
                                               Dunham S.P., Onions D.E.; "The cloning and sequencing of cDNAs encoding two isoforms of feline stem cell factor.";
                                                                                DNA Seq. 6:233-237(1996).

-!-FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).
-!-SUBGNIT: Homodimer, non-covalently linked (Probable).
-!-SUBCELIOLAR LOCATION: Type I membrane protein (isoforms I and 2) Also exists as a secreted soluble form (isoform I only) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G (in
                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR003452; SCF.
PANTHER; PTHR11574; SCF; 1.
Pfam; PF02404; SCF; 1.
Alternative splicing; Cell adhesion; Glycoprotein; Growth factor; Signal; Transmebrane.
SIGNAL
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cycoplasmic (Potential).
N-linked (GlcNAc. .) (Potential).
N-linked (GlcNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
By similarity.
By similarity.
DSRVSVTKPFMLPPVAASSLRNDSSSSNR -> G (
                                                                                                                                                                                                                                                        Isoid=P79169-2; Sequence=VSP 006021; PTM: A soluble form is produced by proteolytic processing of isoform 1 in the extracellular domain (By similarity). SIMILARITY: Belongs to the SCF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tch 87.2%; Score 1217.5; DB 1; Length 274; al Similarity 87.2%; Pred. No. 8.8e-85; 239; Conservative 17; Mismatches 17; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kit ligand.
Extracellular (Potential).
Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C5B78DB4791237BB CRC64;
                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /FTId=VSP 006021
                                                                                                                                                                                                                                   IsoId=P79169-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isoform 2)
                [1]
NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D50833; BAA09445.1; -; mRNA.
SMR; P79169; 29-161.
                                      WEDLINE=97069946; PubMed=8912926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30988 MW;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
Zhang Z., Anthony R.V.;

Zhang Z., Anthony R.V.;

Theorems stem cell factor/c-kit ligand: its molecular cloning and localization within the uterus.";

Biol. Reprod. 50:95-102(1994).

I Biol. Reprod. 50:95-102(1994).

I Biol. Reprod. Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).

I SUBGRILUIAR LOCATION: Type I membrane protein. Also exists as a secreted soluble form (By similarity).

I SUBCALLUIAR LOCATION: Type I membrane protein. Also exists as a secreted soluble form (By similarity).

I PTM: A soluble form is produced by proteolytic processing of the extracellular domain (By similarity).

I SIMILARITY: Belongs to the SCF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-MAX-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
Name-KITLG; Synonyms-MGF;
Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Growth factor; Signal; Transmembrane.
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Kit ligand.

Extracellular (Potential).

Potential.

Cytoplasmic (Potential).

N-linked (GloNAc. .) (Potential).

N-linked (GloNAc. .) (Potential).

N-linked (GloNAc. .) (Potential).

N-linked (GloNAc. .) (Potential).

By similarity.

By similarity.
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CARBOHYD
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                                                                                                                                                                                                                                                                 SEQUENCE
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DT 28-PE
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NUCLECTIOE SEQUENCE.

Yanagisawa N., Tanaka S., Yamanouchi K., Tojo H., Tachi C.;

Yanagisawa N., Tanaka S., Yamanouchi K., Tojo H., Tachi C.;

Yanagisawa N., Tanaka S., Yamanouchi K., Tojo H., Tachi C.;

Yanagisawa N., Tanaka S., Yamanouchi K., Tojo H., Tachi C.;

Yanagisawa N., Tanaka S., Yamanouchi K., Tojo H., Tachi C.;

Yanagisawa N., Tanaka S., Yamanouchi K., Tojo H., Tachi C.;

Yamagisa Yamacin In the brain and the stin of factal solubit and fetal Shiba goats, Capra Hicus.";

Yamacin MaR-1997) to the EMBL/GenBank/DDBJ databases.

Yamanited (MAR-1997) to the EMBL/GenBank databases.

Yamanited (Mar-199
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                                                                              MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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     Gaps
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SMR; Q95M19; 29-161.
InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR003452; SCF.
PANTHER; PTHR11574; SCF; 1.
Pfan; PF02404; SCF; 1.
Cell adhesion; Glycoprotein; Growth factor; Signal; Transmembrane. SIGNAL
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28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2006 (Rel. 47, Last annotation update)
10-MAY-2006 (Rel. 47, Last annotation update)
Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
Name=KITIGS (Goat).
Capra hircus (Goat).
Capra hircus (Goat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi, Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
  Indels
  16;
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22; Mismatches
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  Conservative
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NCBI TaxID=9925;
  235;
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Q95M19;
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TISSUE=Spleen;
MEDLINE=94339176; PubMed=7520283; DOI=10.1016/0167-4889(94)90084-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhou J., Hikono H., Ohtaki M., Kubota T., Sakurai M.; "Cloning and characterization of cDNAs encoding two normal isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Belgian Blue;
MEDLINE=99315331; PubMed=10384045; DOI=10.1007/8003359901076;
Seitz J.J., Schmutz S.M., Thue T.D., Buchanan F.C.;
"A missense mutation in the bovine MGF gene is associated with the roan phenotype in Belgian Blue and Shorthorn cattle.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCF_BOVIN STANDARD; PRT; 274 AA.

028132; 097074;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Name=KITLG; Synonyms=SCF;
Name=KITLG; Synonyms=SCF;
Bos taurus (Bovine)
Eucharia; Laurasiatheria; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                    (Potential).
(Potential).
(Potential).
(Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.0%; Score 1187.5; DB 1; Length 274; 85.0%; Pred. No. 1.7e-82; ive 20; Mismatches 20; Indels 1;
Kit ligand.

Extracellular (Potential).

Potential.

Cytoplasmic (Potential).

N-linked (GlCNAc. . .) (Pote
By similarity.

By similarity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BBFE669A509EF65D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE OF 204-239, AND VARIANT ASP-218
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Biochim. Biophys. Acta 1223:148-150(1994)
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Best Local Similarity 85.0%:
Matches 233; Conservative
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TISSUE-Fetal brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 AA;
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NCBI_TaxID=9913;
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us-10-620-642-61.rup

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180 TKPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKK 239
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                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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TISSUE=T-cell;
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                                                                                                                                                                                                                                                                                                                                                                CANFA
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SCF_CANFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Isola-Q28132-2; Sequence=VSP 006020;
PTM: A soluble form is produced by proteolytic processing of
isoform 1 in the extracellular domain (By similarity).
POLYMORPHISM: The roan locus is responsible for the coat
coloration of Belgian Blue and Shorthorn cattle. The solid-colored
and white animals are homozygotes, and the roan animals, with
intermingled colored and white hairs, are heterozygous. The roan
phenotype is due to the ASP-218 mutation.
SIMILARITY: Belongs to the SCF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKKTQTWIITCIYLQLLFPPLVHTQGICSNRVTDDVKDVKLVANLPKDYMITLKYVPG
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Mamm. Genome 10:710-712(1999).

-!- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).
-!- SUBGNIT: Homodimer, non-covalently linked (Probable).
-!- SUBCLILUIAR LOCATION: Type I membrane protein (isoforms 1 and 2).
Also exists as a secreted soluble form (isoform 1 only) (By similarity).
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(Sytoplasmic (Potential).
(N-linked (GlcNAc. .) (Potential).
N-linked (GlcNAc. .) (Potential).
N-linked (GlcNAc. .) (Potential).
By similarity.
By similarity.
DSRVSVTKPFMLPPVAASSLRNDSSSSNR -> G (in
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84.7%; Pred. No. 2.9e-82;
ive 20; Mismatches 21; Indels 1;
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Extracellular (Potential).
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A -> D (in roan allele).
DGC1DDB77B0CB12B CRC64;
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EMBL; AB033716; BAA94808.1; -; mRNA.
EMBL; AF120154; AAD55355.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q28132-1; Sequence=Displayed;
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274 AA; 31015 MW;
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Best Local Similarity 84.74
Matches 232; Conservative
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SIGNAL
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                  Q06520; Q8SPM6;
Q06520; Q8SPM6;
Q1-UJN-1994 (Rel. 29, Last sequence update)
Q1-UJN-1994 (Rel. 29, Last annotation update)
Mit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast
Cell growth factor) (MGF).
Name-KIITG; Synonyms-MGF;
Canis familiaris (Dog)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Canine stem cell factor (c-kit ligand) supports the survival of hematopoietic progenitors in long-term canine marrow culture."; Exp. Hematol. 20:1118-1124(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=93106145; PubMed=1281786;
Shull R.M., Suggs S.V., Langley K.E., Okino K.H., Jacobsen F.W.,
Martin P.H.;
                                                                       273
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                                                                                                   241 KQPNLTRTVENRQINEEDNEISMLQEKEREFQEV
                                                                       240 RQPSLTRAVENIQINEEDNEISMLQEKEREFQEV
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InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR003452; SCP
PANTHER; PTHR11574; SCF; 1.
Pfam; PF02404; SCF; 1.
Cell adhesion; Glycoprotein; Growth f
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EMBL; AY094361; AAM16280.1; -; mRNA.
PIR; 146229; 146229.
SRR; Q06220; 29-161.
Ensembl; ENSCAFG00000006091; Canis fa
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NCBI_TaxID=9606;
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CONFLICT
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CARBOHYD
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068D22 HUM
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                                                                                                                                                                                                                                                                                                                                     KOLKKSPKSPEPRLFTPEEFFRIFNRSIDAFKOF-VVASETSOCVVSSTLSPEKOSRVSV 179
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955N18; OS5NNS;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 41, Last sequence update)
Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).

Name=KTILG; Synonyms=SCF;
Mustela vison (American mink).
Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Mustelidae; Mustelinae; Mustelinae; Musteliae
                                                                                                                                                                                                                          MDVLPSHCWISVWVEQLSVSLTDLLDKFSNISEGLSNYSIIDKLVKIVDDLVECTEGYSF
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(Potential).
(Potential).
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                                                                                                                                                                         1,
                                                                                                                                          84.5%; Score 1180.5; DB 1; Length 274; 85.4%; Pred. No. 5.9e-82; ive 17; Mismatches 22; Indels 1;
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Thm: A soluble form is produced by proteolytic processing
isoform 1 in the extracellular domain (By similarity).
SIMILARITY: Belongs to the SCF family.
                                                                                                              4182BE9AED00793B CRC64;
Cytoplasmic (Potential).
N-linked (GlCNAc. . ) (PN-linked (GlCNAc. . ) (PN-linked) (GlCNAc. . ) (PN-linked)
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Name=1;
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NUCLECTIDE SEQUENCE (ISOFORMS 1 AND 2).
                                                                                                              MW,
                                                                                                                                        Query Match
Best Local Similarity 85.4%
Matches 234; Conservative
                                                                                                              30870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
 274
90
97
145
114
114
 239 2
90 97
145 1
196 1
29 1
68 1
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TOPO DOM
CARBOHYD
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SEQUENCE
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the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
470-0CT-2004 (TrEMBLrel. 28, Last annotation update)
470-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Name=DKFZp686F2250;
Nam
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (in Ref
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kit ligand.

Extracellular (Potential).

Extracellular (Potential).

Cytoplasmic (Potential).

N-linked (GlCMAc. .) (Potential).

N-linked (GlCMAc. .) (Potential).

N-linked (GlCMAc. .) (Potential).

N-linked (GlCMAc. .) (Potential).

By similarity.

By similarity.

DSRYSVTKPPMLPPVAASSLRNDSSSSNR -> G (S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adhesion; Glycoprotein; Growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isoform 2).
/FTId=vSP 006024.

S -> P (in Ref. 1; AAK73366).
S -> N (in Ref. 1; AAK73366).
S -> N (in Ref. 1; AAK73366).
EREFQEV -> RESFKRCNCGFYHTVLSYLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.5%; Score 1180.5; DB 1; Length 274; 84.3%; Pred. No. 5.9e-82; ive 20; Mismatches 22; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5AC1619014AE5E72 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                           SMR; Q95NB; 29-161.
InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR012351; Cytokine_4_hlx.
InterPro; PR012351; SCF.
PANTHER; PTR11574; SCF; 1.
Pfam; PF02404; SCF; 1.
Alternative splicing; Cell adhesion; G
Signal; Transmenbrane.
SIGNAL
                                                                                                                                                                                                                                                                                                                    EMBL; AY013712; AAG37434.1; -; mRNA.
EMBL; AF323757; AAK73366.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              274 AA; 31035 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P21581; Q9QWZ4; Q9Z2E7;
01-MAY-1991 (Rel. 18, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF) (Hematopoietic growth factor KL).
Name=Ktilg; Synonyms=MGF;
Rattus norvegicus (Rat)
Rattus norvegicus (Rat)
Mammalia; Butheria; Buzrchontoglires; Giires; Rodentia; Sciurognathi; Muroidea; Murinae; Rattus.
                                                                                                                                                                                                                                             44 VANLPKDYMITLKYVPGMDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDK
                                                                                                                                                                                                                                                                                             LVNI VDDLVECVKENSSKDLKKS FKSPEPRLFTPEEFFRI FNRS I DAFKDFVVASETSDC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE OF 1-201, AND PARTIAL PROTEIN SEQUENCE.
MEDLINE=91004219; PubMed=2208279; DOI=10.1016/0092-8674(90)90301-T;
MARTIN F.H., Sugges S.V., Langley K.E., Lu H.S., Ting J., Okino K.H.,
Morris C.F., McNiece I.K., Jacobsen F.W., Mendiaz E.A., Birkett N.C.,
Smith K.A., Johnson M.J., Parker V.P., Flores J.C., Patel A.C.,
Fisher E.F., Erjavec H.O., Herrara C.J., Wypych J., Sachdev R.K.,
Pope J.A., Leslie I., Wen D., Lin C.-H., Cupples R.L., Zsebo K.M.;
"Primary structure and functional expression of rat and human stem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFIDE
                                                                                                                                                                                                                     Gaps
                           Ottenwaelder B., Obermaier B., Deutschenbaur S., Schaipp A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR749222; CAH18078.1; -; MRNA.
SWR; Q68DZ2; 9-126.
GO; GC:001620; G::membrane; IEA.
GO; GO:0005173; F:stem cell factor receptor binding; IEA.
GO; GO:0005173; F:stem cell factor receptor binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                         PSLIIGFAFGALYWKKRQPSLTRAVENIQINEEDNEISMLOEKEREFQEV 273
                                                                                                                                                                                                                     ;
                                                                                                                                                                                             83.8%; Score 1171; DB 2; Length 238; 100.0%; Pred. No. 2.6e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN SEQUENCE OF 26-190, CARBOHYDRATE-LINKAGE SITES, AND
                                                                                            GC:0016620; C:membrane; IEA.
GO:0005173; F:stem cell factor receptor binding; IEA
GO:0007155; P:cell adhesion; IEA.
                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).
Teramoto T., Nagashima M., Thorgeirsson S.S.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRIN-Buffalo; TISSUE-Liver;
MEDLINE-91217037; PubMed-1708771;
Lu H.S., Clogston C.L., Mypych J., Fausset P.R., Lauren
                                                                                                                                                                      238 AA; 26667 MW; 7D6B1E487BE3709B CRC64;
                                                                                                                                                                                                    100.0%; Pred. No. -ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
           TISSUE=Amygdala;
The German cDNA Consortium;
                                                                                                                                InterPro; IPR003452; SCF.
Pfam; PF02404; SCF; 1.
                                                                                                                                                                                                                     Matches 230; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell factor DNAs.";
Cell 63:203-211(1990)
                                                                                                                                                            protein.
SEQUENCE.
                                                                                                                                                                                                         Similarity
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                                                                                                                                                        Hypothetical
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R EMBL; AF071205, AAD02828.1; -; mRNA.

R EMBL; M59966; AAA42117.1; -; mRNA.

R PSTS B35974; B35974; B35974;

R ENSEMBL; 29-159.

R ENSEMBL; ENSRNOG00000005386; Rattus norvegicus.

R InterPro; IPR012351; Cytokine_4_hlx.

InterPro; IPR013452; SCF.

R PANTHER; PTH11574; SCF; 1.

R PANTHER; PTH11574; SCF; 1.

R Pfam; PF03404; SCF; 1.

Alternative splicing; Cell adhesion; Direct protein sequencing; M Glycoprotein; Growth factor; Pyrrolidone carboxylic acid; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                         TUNCTION: Stimulates the proliferation of mast cells. Able to FUNCTION: Stimulates the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins.

SUBGUNIT: Homodimer, non-covalently linked (Probable).

SUBGINIT: Homodimer, non-covalently linked (Probable).

SUBGILLUAR LOCATION: Type I membrane protein (isoforms 1 and 2) Also exists as secreted soluble form (isoform 1 only) (By similarity).
                                                                                                                                                      PROTEIN SEQUENCE OF 26-39.
MEDLINE=91004218; PubMed=2208278; DOI=10.1016/0092-8674(90)90300-4; Zsebo K.M., Wypych J., McNiece I.K., Lu H.S., Smith K.A., Karkare S.B., Sachdev R.K., Yuschenkoff V.N., Birkett N.C., Williams L.R., Satyagal V.N., Tung W., Bosselman R.A., Mendiaz E.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -> G (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=2; Synonyms=KL-2; ISO 000025; ISOId=P21581-2; Sequence=VSP 006025; ISOId=P21581-2; Sequence=VSP 006025; DEVELOPMENTAL STACE: Acts in the early stages of hematopoiesis. PTM: A soluble form is produced by proteolytic processing of isoform 1 in the extracellular domain. SIMILARITY: Belongs to the SCF family.
Mendiaz E.A., Zsebo K.M., Langley K.E.;
"Amino acid sequence and post-translational modification of stem cfactor isolated from buffalo rat liver cell-conditioned medium.";
J. Biol. Chem. 266:8102-8107(1991).
                                                                                                                                                                                                                                                                                                            Langley K.E.; "Identification, and biological characterization of hematopoietic stem cell factor from buffalo rat liver-conditioned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cycollasmic (Potential).
Pyrrolidone carboxylic acid.
N'linked (GlCNAc. .); partial.
N-linked (Brobable).
O-linked (Probable).
O-linked (Probable).
N-linked (Probable).
N-linked (GlCNAc. .); partial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSRVSVTKPFMLPPVAASSLRNDSSSSNR
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/FTId=VSP 006025.
S -> P (in Ref. 1; AAD02828).
C0P56527DC93FD27 CRC64;
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Extracellular (Potential)
Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=1; Synonyms=KL-1;
IsoId=P21581-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30712 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALTERNATIVE PRODUCTS:
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273 AA;
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                                                                                                             MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                              KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                         KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 240
                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular cloning of mast cell growth factor, a hematopoietin that is active in both membrane bound and soluble forms.";
                                                                  MKKTQTWILITCIYLQLLLFNPLVKTBGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE (ISOFORM 1).
MEDLINE-3012240; PubMed=1381087;
Brannan C.I., Bedell M.A., Resnick J.L., Eppig J.J., Handel M.A.,
Williams D.E., Lyman S.D., Donovan P.J., Jenkins N.A., Copeland N.G.,
"Developmental abnormalities in Steell7H mice result from a splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-92330001; PubMed=1378327;
Huang E.J., Nocka K.H., Buck J., Besmer P.;
"Differential expression and processing of two cell associated forms
of the kit-ligand: KL-1 and KL-2.";
Mol. Biol. Cell 3:349-362(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=WCBGF1;
MEDLINE=91160046; PubMed=1705866; DOI=10.1016/0092-8674(91)90326-T;
Rlanagan J.G., Chan D.C., Leder P.;
"Transmembrane form of the kit ligand growth factor is determined by alternative splicing and is missing in the Sld mutant.";
Cell 64:1025-1035(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=WCB6F1;
MEDLINE=91004223; PubMed=1698558; DOI=10.1016/0092-8674(90)90304-W;
Anderson D.M., Lyman S.D., Baird A., Wignall J.M., Eisenman J.,
Rauch C., March C.J., Boswell H.S., Gimpel S.D., Cosman D.,
Williams D.E.;
                                                                                                                                                                                                                                                                                                                          P20826; P97332; Q62524; Q64222; Q921N5; O1-FEB-1991 (Rel. 17, Created) (1-MAY-1991 (Rel. 18, Last sequence update) (1-MAY-2005 (Rel. 47, Last annotation update) (Stel. 47, Last annotation (Stem cell factor) (SCF) (Mast cell growth factor) (MGF) (Hematopoletic growth factor KL) (Steel
                                 ö
          Length 273;
                                 30; Indels
         Score 1158; DB 1;
Pred. No. 3.1e-80;
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                                                                                                                                                                                                                                       QPSLTRAVENIQINBEDNEISMLQEKEREFQEV 273
                                                                                                                                                                                                                                                                                                                      273 AA
                               18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            Name=Kitlg; Synonyms=Kitl, Mgf, Sl, Slf;
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         sch 82.9%;
il Similarity 82.4%;
225; Conservative 1
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        Query Match
Best Local S:
Matches 225
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RECORDED SECURNCE [LARGE SCALE MRNA] (ISOFORM 1).

RECORDED SECURNCE [LARGE ST. Adachi J., Bono H., Kondo S., RA OKAZAKI Y., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Balade J., Franch D. Brusic V., Corbani D. B., Quackenbush J. A., Balade J., Ranada D. Brusic V., Chochia C., Corbani D. B., Cousins S., Balake J.A., Braded D., Brusic V., Chochia C., Corbani D. B., Cousins S., Dalla B., Dragami T.A., Fletcher C.F., Forrest A., Frazer K.S., Gasterland T., Garboddi M., Gissi C., Godzik A., Gard B. E., Cousins S., Armai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Ranachandran S., Ronagaya A., Numata K., Okido T., Pavan Maglott D.R., Maltais L., Marchhomi D., McKenie L., Miki H., Rawasi T., Reed J.C., Reed D.J., Reid J., Ranachandran S., Sandelin A., Schneider C., Semple C.A., Setou M., Shinama K., Takenaka Y., Taylor M.S., Tanadale R.D., Tomita M., Shinana K., Watanabe Y., Hayatsu N., Ranachanda K., Watanabe L., Wahlestedt C., Wang Y., Watanabe Y., Hayatsu N., Rayazaki A., Sakai K., Kawai J., Ronno H., Nakamura M., Sakazume N., Sako K., Alaxa A., Hashizume W., Imotani K., Inbhi Y., Itoh M., Kagawa I., Raunak R., Hashizume W., Imotani K., Inbhi Y., Itoh M., Kagawa I., Haranaki R., Washizaki A., Sakai K., Sasaki D., Shibata K., Shibata K., Shinagawa B., Ranachi, R., Shibata K., Shinagawa B., Ranachi, R., Shibata K., Shibata K., Shinagawa B., Ranachi, R., 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [6]
NUCLECTIDE SEQUENCE (ISOFORM 1), AND VARIANTS PRO-193 AND SER-207.
STRAIN-C3H/E1; TISSUE-Brain;
STRAINE-31/213534; PubMed=8875893; DOI=10.1007/8003359900247;
Graw J., Loester J., Neuhaeuser-Klaus A., Pretsch W., Schmitt-John "Molecular analysis of two new Steel mutations in mice shows a transversion or an insertion.";
Mamm. Genome 7:843-846(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE (ISOFORM 1), AND VARIANTS SER-122; PRO-193 AND
                                                                                                                                                                                                                                                                                  Bedell M.A., Copeland N.G., Jenkins N.A.; "Multiple pathways for Steel regulation suggested by genomic and sequence analysis of the murine Steel gene."; Genetics 142:927-934 (1996).
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in the steel factor cytoplasmic tail.";
                                                                                                                                                                                                   STRAIN=C57BL/6J;
MEDLINE=97002551; PubMed=8849898
                                                                                                                                              NUCLEOTIDE SEQUENCE (ISOFORM 1)
                                               Genes Dev. 6:1832-1842(1992)
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Mutat. Res. 382:75-78(1997)
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Cytokine 11:249-256(1999).
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          M59915;
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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villadon D.K., Muzny D.M., Sodergren E.J., Lux K., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.M., Kzzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Green L.D., Grimwan d. M., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A.,
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MEDLINES-91004216; PubMed=1698554; DOI=10.1016/0092-8674(90)90298-S;

MEDLINES-91004216; PubMed=1698554; DOI=10.1016/0092-8674(90)90298-S;

Copeland N.G., Gilbert D.J., Cho B.C., Donovan P.J., Jenkins N.A.,

Cosman D., Anderson D., Lyman S.D., Williams D.E.;

"Mast cell growth factor maps near the steel locus on mouse chromosome
10 and is deleted in a number of steel alleles.";

Cell 63:175-183(1990)
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MEDIJNE=91004220; PubMed=1698556; DOI=10.1016/0092-8674(90)90302-U; Z8ebO K.M., Williams D.A., Gelseler E.N., Broudy V.C., Martin F.H., Atkins H.L., Hsu R.-Y., Birkett N.C., Okino K.H., Murdock D.C., Jacobsen F.W., Langley K.E., Smith K.A., Takeishi T., Cattanach B.M., Galli S.J., Sugss S.V.;
"Stem cell factor is encoded at the Sl locus of the mouse and is the ligand for the c-kit tyrosine kinase receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell 63:157-174(1990).

-I- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins.
-I- SUBGURIT: Homodimer, non-covalently linked (Probable).
-I- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).
-I- SUBCELLULAR is as a secreted soluble form (isoform 1 only) (By similarity).
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MEDLINE=91004215; PubMed=1698553; DOI=10.1016/0092-8674(90)90297-R; Williams D.E., Eisenman J., Baird A., Rauch C., van Ness K., March C.J., Park L.S., Martin U., Mochizuki D.Y., Boswell H.S., Burgess G.S., Cosman D., Lyman S.D.; "Identification of a ligand for the c-kit proto-oncogene.";
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                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE OF 1-270 (ISOFORM 1), AND PROTEIN SEQUENCE
                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Name=1; Synonyms=KL-1;
IsoId=P20826-1; Sequence=Displayed;
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SUBGNIT: Homodimer, non-covalently linked (Probable).
SUBGRILULAR LOCATION: Type I membrane protein. Also exists as a
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAX-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast call growth factor) (MGF) (Fragment).
Name-KITLG; Synonyms-SCF;
Ovis aries (Sheep).
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MEDLINE-99263397; PubMed=10328863; DOI=10.1006/cytc.1998.0430;
MEDLINE-99263397; PubMed=103288639; DOI=103288639;
MEDLINE-99263997; PubMed=103288639; DOI=1032888639; DOI=1032888639; DOI=1032888639; DOI=1032888639; DOI=1032888639; DOI=1032888639; DOI=1032888639; DOI=1032888639; DOI=10328888639; DOI=10328888888889; DOI=103288888889; DOI=1032888888888889; DOI=10328888888888
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Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
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MEDLINE-9641380; PubMed 6662240; DOI=10.1007/s003359900142;
Tisfall D.J., Quirke L.D., Galloway S.M.;
"Ovine stem cell factor gene is located within a syntenic group
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome 3 conserved across mammalian species.";
Mamm. Genome 7:472-473(1996).
M57647; AAA39538.1; -; mRNA.
840534; ABA22555.2; -; mRNA.
V68989; CAA48778.1; -; mRNA.
U44724; -; NOT ANNOTATED CDS; Genomic_DNA.
U44725; AAC52447.1; -; mRNA.
X95381; CAA64667.1; -; mRNA.
X99322; CAA67698.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1157; DB 1;
Pred. No. 3.7e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 OPSLTRAVENIQINEEDNEISMLOEKEREFQEV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pecora; Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE OF 8-267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.8%;
82.8%;
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61 MDVLPSHCWLRDMVTHLSVSLTTLLDKFSNISEGLSNYSIIDKLGKIVDDLVACMEBNAP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKKTQTWIITCIYLQLLLFNPLVKTQEICRNPVTDNVKDIIKLVANLFNDYMITLNYVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
                                                                                                                                                                                                                                                                                                                                                                                    1 MKKTQTWILTCIYLQLLLPNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  two cell associated forms
[1]
NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SPIRATINESPIRATION TISSUB-Embryonic Kidney;
MEDLINE-22831116; PubMed=12951073; DOI=10.1016/j.bbrc.2003.08.025;
HITOKAWA Y.S., Watanabe M., Shiraishi T.;
HITOKAWA Y.S., Watanabe M., Shiraishi T.;
cotransfected vector.
                                                                                                                                                                                                                                                                                                                                  28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                           Query Match 71.0%; Score 992; DB 2; Length 245
Best Local Similarity 71.8%; Pred. No. 1.3e-67;
Matches 196; Conservative 18; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
C-kit ligand C-terminally truncated secreted form KL-Sld.
Name=Kitl;
                                                                                                                                                                       Biochem. Biophys. Res. Commun. 309:469-474(2003).
EMBL; AB105879; BAC84980.1; -; mRNA.
SEQUENCE 245 AA; 27681 MW; 9615130876AC9D52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23222 MW; C74DD639566EB817 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q64384_9MURI PRELIMINARY;
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SEQUENCE 208 AA; 2:
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                                                                                                                      This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Growth factor; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Potential).
(Potential).
(Potential).
secreted soluble form (By similarity).

PTM: A soluble form is produced by proteolytic processing of extracellular domain (By similarity).

SIMILARITY: Belongs to the SCF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ξ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fotential.

Kit ligand.

Extracellular (Potential).

Potential.

Cytoplasmic (Potential).

Ninked (GIONAc. ..) (Pote
N-linked (GIONAc. ..) (Pote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW; 9D9D959E4B9EC841 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.8%; Score 1156.5; DB
85.0%; Pred. No. 3.9e-80;
ive 19; Mismatches 20
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                                                                                                                                                                                                                                                                                                                        PIR; SS8313; SS8313.
SWR; P79368; 29-161.
InterPro; IPR012351; Cytokine 4 hlx.
InterPro; IPR013452; SCF.
PAWTHER; PTHR11574; SCF; 1.
Pfam; PF02404; SCF; 1.
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                                                                                                                                                                                                                                                                           EMBL; U89874; AAB49491.1; -; mRNA.
EMBL; Z50743; CAA90620.1; -; mRNA.
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Q54A14;
13-SEP-2005 (TrEMBLrel. 31, C:
13-SEP-2005 (TrEMBLrel. 31, Li
13-SEP-2005 (TrEMBLrel. 31, Li
Stem cell factor KL-2.
Name=scf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 55.0%;
Matches 227; Conservative
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215
238
>267
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267 AA;
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DISULFID
DISULFID
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TRANSMEM
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CARBOHYD
CARBOHYD
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054A14 RAT
10 054A14
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DT 13-SEP
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Db 1 MKKTQTWIITCIYLQLLENPLVKTKEICGNPVTDNVKDITKLVANLENDYMITLNYVAG 60

Cy 61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120

Cy 121 KDLKKSFKSPEPFRLFTFLENFSNISEGLSNYSIIDKLVNDLVCKEENAP 120

Cy 121 KDLKKSFKSPEPFRLFTFRSIDAFKDFVVASETSDCVVSSTLGPEKDSRVSVT 180

121 KDLKKSFKSPEPFRIFTRSIDAFKDFVVASETSDCVLSSTLGPEKDSRVSVT 180

Cy 181 KPFMLPPVAASSLRNDSSSNRKA 204

Db 181 KPFMLPPVAASSLRNDSSSNRKA 204

Search completed: February 22, 2006, 18:19:21

Job time: 141.636 sees
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Sequence Sequence Sequence

Sequence

Sequence Sequence Sequence Sequence

Sequence Sequence

Sequence

Sequence Sequence Sequence Sequence Sequence

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Database :

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1 MKKTOTWILTCIYLOLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08220379B
Patent No. 5525708
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IDN COMPATIBLE
COMPUTER: ISN PC COMPATIBLE
COMPUTER: ISN PC COMPATIBLE
COMPUTER: ISN PC COMPATIBLE
COMPATING SYSTEM: PC-DS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,379B
FILING DATE: 28-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HALBY Jr. James F
REGISTRATION NUMBER: 27,794
REFERENCE/POCKET NUMBER: CytoMed/2
TELEPHONE: 212-596.9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 1397; DB 1;
100.0%; Pred. No. 4.9e-134;
iive 0; Mismatches 0;
US-08-336-728A-50
US-08-955-848A-82
US-08-482-918-57
US-09-224-681-57
US-09-635-251-57
US-09-604-325A-57
US-09-604-325A-57
US-09-604-325A-63
US-09-336-728A-63
US-09-336-728A-63
US-09-635-531-63
US-09-635-63
US-09-635-63
US-09-635-63
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US-09-649-63
US-09-635-63
US-09-635-63
US-09-635-63
US-09-635-63
US-09-635-63
US-09-648-635-63
US-09-949-016-9391
US-09-949-016-9391
US-09-948-635-63
US-09-948-016-9391
                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cleavage site
164..165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 273 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 273; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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LOCATION:
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                                                                                                      February 22, 2006, 18:19:42; Search time 33.0909 Seconds (without alignments) 682.074 Million cell updates/sec
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                                                                                                                                                                                               1 MKKTQTWILTCIYLQLLLFN.....NBEDNBISMLQEKERBFQEV 273
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Biocceleration Ltd.
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/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTuS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-09-224-681-49
US-09-224-681-61
US-08-336-728A-48
US-08-336-728A-49
US-08-336-728A-61
US-08-336-728A-61
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US-09-224-681-50
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                                                                                                                                                                                                                                                                        572060 segs, 82675679 residues
                  version -
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Maximum Match 100%
Listing first 45 summaries
                                                                          protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                  GenCore (c) 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                          Issued Patents AA:*
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Maximum DB seq length: 200000000
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1397
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Match Length
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Score

Result

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1 MKKTQTWILICIYLQLLLENPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60

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Sequence

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XOLKKSPKSPEPRLFTPEEFFRIFURSIDAFKDFVVASETSDCVVSSTLSPEKOSRVSVT 180
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KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                         181 KPFMLPPVAASSIRNDSSSSNRKAKNPPGDSSIHWAAMALPALFSLIIGFAFGALYWKKR 240
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                                                                                      KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUR SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-UN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                    241 QPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
                                                                                                                                                                           241 OPSLTRAVENIQINEEDNEISMLOEKEREFOEV 273
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APPLICANT: Zeebo, Krisztina M.
APPLICANT: Bugge, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstei
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STATE: Illinois
COUNTRY: United States of America
ZIP: 6060-6402
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Patent No. 6207417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INPORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFRENCE/DOCKET NUMBER: 0101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
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Best Local Similarity 100.
Matches 273; Conservative
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US-08-482-918-49
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1-248 SCF protein begins at amino acid 26; amino acid 1-25
include Met and leader sequences for membrane band form of
recombinant SCF."
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                           61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                               121 KDLKKSPKSPEPRLFTPEEFPRIFNRSIDAFKDPVVASETSDCVVSSTLSPEKDSRVSVT 180
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APPLICANT: Lu, Haieng
TITLE OF INVENTION: SCF ANALOG COMPOSITIONS AND METHODS
NUMBER OF SECURNCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA

ZIP: 91320-1789

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,428
FILING DATE: 05-APR-1996
FILING DATE: 05-APR-1996
ATTONREY/AGENT INFORMATION:
NAME: Knight, Matthew W
REGISTRATION NUMBER: 36,846
REFERENCE/DOKET NUMBER: 36,846
REFERENCE/DOKET NUMBER: 36,846
REFERENCE/DOKET NUMBER: A-400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: TYPE: Innear
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100.0%; Pred. No. 4.9e-134;
ive 0; Mismatches 0;
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STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
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Best Local Similarity 100.
Matches 273; Conservative
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OTHER INFORMATION:
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OTHER INFORMATION:
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STATE: CA
COUNTRY:
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                        181 KPFMLPPVAASSLRNDSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 240
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181 KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 240
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                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zebo, Krisztina M.
APPLICANT: Zebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Busselman, Robert A.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago Sars Tower, 233 South Wacker Drive STATE: 111nois CUNTRY: United States of America 21P: 60606-6402 COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPATIBLE PREADABLE PROBY MS-DOS SOFTWARE: Patentln Release #1.0, Version #1.30 SOFTWARE: Patentln Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/482,918 FLING DATE: 07-401-1995 CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION: NAME: Clough, David W. REGISTRATION NUMBER: 36,107 REFERENCE/DOCKET NUMBER: 01017/33005 TELECOMMUNICATION INFORMATION: METERSERICE/DOCKET NUMBER: 01017/33005
                                                                                                                                   241 QPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
                                                                                                     241 OPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 61: SEQUENCE CHARACTERISTICS: LENGTH: 273 amino acids TYPE: amino acids TOPOLOGY: linear
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TELEFAX: 312/474-0448
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Best Local Similarity 100.0
Matches 273; Conservative
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US-08-482-918-61
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US-09-224-681-61

US-09-224-681-61

US-09-224-681-61

Sequence 61, Application US/09224681

Patent No. 2507454

GENERAL INFORMATION:

APPLICANT: Seebo, Krisztina M.

APPLICANT: Bosselam, Robert A.

APPLICANT: Wartin, Francis H.

ITILE OF INVENTION: Wethod for Enhancing the Efficiency of Gene

TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide

CORRESPONDENCE ADDRESS:

ADDRESSEE Marshall O'Toole Geretein Murray & Borun

STREET: GAOG Sears Tower, 233 South Wacker Drive

CONFERS READALE FORM:

MEDION TYPE: ILING SARIES OF America

COMPUTER READALE FORM:

MEDION TYPE: BORN:

COMPUTER READALE FORM:

MEDION TYPE: BORN:

COMPUTER READALE FORM:

MEDION TYPE: BORN:

MEDION TYPE: BORN:

COMPUTER READALE TOWN

COMPUTER: BATCATION DATA:

APPLICATION NUMBER: 09/005,893

CLASSIFICATION NUMBER: 09/005,893

FILING DATE: 12-DAN-1995

FILING DATE: 12-DAN-1995

FILING DATE: 12-DAN-1995

FILING DATE: 01-CT-1900

PRIOR APPLICATION NUMBER: 07/589,701

PRIOR APPLICATION NUMBER: 07/589,701

PRIOR APPLICATION NUMBER: 07/537,198

FILING DATE: 11-UND-1990

FILING DATE:
                                                                                                                                                                                                                         181 KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 240
                                                                                                           KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
Query Match 100.0%; Score 1397; DB 2; Length 273; Best Local Similarity 100.0%; Pred. No. 4.9e-134; Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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US-516-316-728A-48B

Sequence 48, Application US/08336728A

Patent No. 6207802

GENERAL INFORMATION:

APPLICANT: Scebo, Krisztina M.
APPLICANT: Sugga, Sidney V.
APPLICANT: Bosselman, Robert A.
APPLICANT: Martin, Francis H.

ITILE OF INVENTION: Stem Cell Factor

NUMBERS OF SEQUENCES:
ADDRESSE:
ADDR
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100.0%; Score 1397; DB 2;
Best Local Similarity 100.0%; Pred. No. 4.9e-134;
Matches 273; Conservative 0; Mismatches 0;
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APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acide
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            // TOPOLOGY: linear
// MOLECULE TYPE: protein
US-09-224-681-61
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1 MKKTOTWILTCIYLQLLLENPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSITCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 10-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY AGENT INFORMATION:
NAME: Clough, David W.
RERERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 QPSLTRAVENIQINBEDNEISMLQEKEREFQEV 273
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US-08-336-728A-61
; Sequence 61, Application US/08336728A
; Patent No. 6207802;
; GENERAL INFORMATION:
; APPLICANT: Zeebo, Krisztina M.
; APPLICANT: Sugge, Sidney V.
           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELERAX: 312/4/4-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
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TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKKTQTWILTCIYLQLLLENPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
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Patent No. 6207802
GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Buggs, Sidney V.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marchall, O'Toole, Gerstein, Murray & Bor
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1397; DB 2;
100.0%; Pred. No. 4.9e-134;
tive 0; Mismatches 0;
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PILING DATE: 25-NOV-1992

PRICK APPLICATION DATA:

PAPLICATION NUMBER: 07/589,701

FILING DATE: 01-0CT-1990

PRIOR APPLICATION DATA:

PILING DATE: 24-AuG-1990

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: 07/42,383

FILING DATE: 11-0UN-1990

PRIOR APPLICATION NUMBER: 07/42,383

FILING DATE: 16-0CT-1989

ATTORNEY/AGENT INFORMATION:

NAME: Clough, David M.

REGISTRATION NUMBER: 36,107

REGISTRATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFRENCE: 312/474-6300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 273; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-336-728A-48
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US-08-336-728A-49
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0; Gaps 0;

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61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                      APPLICANT: Zeebo, Krisztina M.
Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSER: ANSTABAll, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 4.9e-134;
Matches 273; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Chicago

STATE: 111inois

COMPUTRY: United States of America

COUNTRY: United States of America

ZIP: 6606-6402

COMPUTER: EADABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: IBM PC compatible

OPERATION SYSTEM: PC-DOS/MS-DOS

SOFTWARR: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/635,251

FILING DATE: 07-Aug-2000

CLASSIFICATION NUMBER: 08/449,182

FILING DATE: 24-AMR-1992

APPLICATION NUMBER: 08/172,329

FILING DATE: 21-DEC-1993

APPLICATION NUMBER: 07/684,535

FILING DATE: 21-DCT-1991

APPLICATION NUMBER: 07/59,701

FILING DATE: 04-OCT-1991

APPLICATION NUMBER: 07/59,719

FILING DATE: 11-JUN-1990

APPLICATION NUMBER: 07/537,198

FILING DATE: 11-JUN-1990

APPLICATION NUMBER: 07/642,383

ATTORNEY/AGENT INFORMATION:

NAME: Clough, David W.

REFERENCE/DOCKET NUMBER: 01017/32957A

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-09-635-251-49
                                                                                                                      ; Sequence 49, Application US/09635251; Patent No. 6759215; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
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TELEFAX: 312/474-0448
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INFORMATION FOR SEQ ID NO: 49:
                                                                RESULT 10
US-09-635-251-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
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                                                                                                                             E: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                      STREET: bajou seats accerding the converge of the cago of the cago
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APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerst
STREET: 6300 Sears Tower, 233 South
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TYPE: linear
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-336-728A-61
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121 KOLKKSPEKPERPERPERPERPERPRIENTSIDAPKOPVVASETSDCVVSSTLSPEKOSRVSVT 180
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                                                                                                                                                                                                           KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
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                                                                                                             Length 273;
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ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
CITY: Chicago
STATE: Chicago
STATE: United States of America
COWITY: United States of America
ZIP: 6066-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/224,683
                                                                                                           Query Match
100.0%; Score 1397; DB 2; Length;
Best Local Similarity 100.0%; Pred. No. 4.9e-134;
Matches 273; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Sugge, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 OPSLITRAVENIOINEEDNEISMLOEKEREFOEV 273
        h MOLECULE TYPE: protein
i SEQUENCE DESCRIPTION: SEQ ID NO: 61:
US-09-635-251-61
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PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/49,653
FILING DATE: 24-MAY-1995
CLASSIFICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/599,701
FILING DATE: 01-0CT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/593,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
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US-09-224-683-49
; Sequence 49, Application US/09224683
; Patent No. 6841147
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISBGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                121 KOLKKSPKSPEPRLFTPEEFFRIFNRSIDAFKOFVVASETSOCVVSSTLSPEKOSRVSVT 180
                                                                                                                                                                                181 KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGPAFGALYWKKR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 6056-6402
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OORFWING SYSTEM: PC-DOS/WS-DOS
CORFWING SYSTEM: NC-DOS/WS-DOS
CORFWING SYSTEM: BC-DOS/WS-DOS
CORFWING SYSTEM: US/O9/635,251
FILING DATE: 07-Aug-2000
CLASSIPICATION NUMBER: 08/49,182
FILING DATE: 25-MOY-1995
APPLICATION NUMBER: 08/49,182
FILING DATE: 25-MOY-1992
APPLICATION NUMBER: 07/684,535
FILING DATE: 25-MOY-1992
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 01-OCT-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 16-OCT-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 16-OCT-1999
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/537,198
                                                                                                                                                                                                                                                                                   NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REPERENCE/DOCKET NUMBER: 01017/32957A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bosselman, Robert A. Suggs, Sidney V. Martin, Francis H. TITLE OF INVENTION: Stem Cell Factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 61, Application US/09635251
Patent No. 6759215
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
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LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
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TELEFAX: 312/474-0448
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGPAFGALYWKKR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKXVPG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 1397; DB 2; Length 273; Best Local Similarity 100.0%; Pred. No. 4.9e-134; Matches 273; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Marchall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chloago STATE: 11linois COUNTRY: United States of America COMPUTER READABLE FORM: PC-DOS/MS-DOS SOFTWARE: BAP PC COMPATIBLE COMPUTER: BAP PC COMPATIBLE PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/224,683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-224-683-61
Sequence 61, Application US/09224683
Sequence 61, Application US/09224683
Sequence 61, Application US/09224683
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Martin, Francis H.
TILE OF INVENTION: Stem Cell Factor: Composition Claims NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
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3R: 01017/35136
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/42,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/3:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LEMOTH: 273 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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121 KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 KOLKKSFKSPEPRLFTPEBFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKKTQTWILICIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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US-09-604-325A-49
; Sequence 49, Application US/09604325A
; Patent No. 6852313
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
Bosselman, Robert A.
                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION ALA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/527,383
FILING DATE: 16-OCT-1989
ATTORNEY AGENT INFORMATION:
NAMB: CLOUGH, DAVIG M
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 36,107
RELEPHONE: 312/474-6300
TELLEPAN: 312/474-6300
TELLEPAN: 25-3856
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH 273 amino acids
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/00
FILING DATE: 12-JAN-1998
CLASSIPICATION:
PRIOR APPLICATION DATA:
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amino acid
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; MOLECULE TYPE: protein
US-09-224-683-61
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RESULT 15
US-09-604-325A-61
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                                                                                                   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                     CITY: Chicago
STATE: 11linois
COUNTRY: United States of America
ZIP: 6666-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: ParentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/604,325A
FILING DATE: 17-Jun-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-CT-1990
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/573,198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32953
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFRAX: 312/474-0448
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INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
STRANDEDNESS: single
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-09-604-325A-49
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 11-JUN-1990
APPLICATION WINGBER: 07/422,383
FILING DATE: 16-0CT-1989
ATTORNEY/AGENT INFORMATION:
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180 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKCVNIVDDLVBCVKENSS 120 181 KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 240 61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS KDLKKSPKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKXVPG KOLKKSPKSPBPRLFTPBBFPR1FNRSIDAFKDFVVASBTSDCVVSSTLSPBKDSRVSVT 1 MKKTQTWILICIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive ô Query Match 100.0%; Score 1397; DB 2; Length 273; Best Local Similarity 100.0%; Pred. No. 4.9e-134; Matches 273; Conservative 0; Mismatches 0; Indels 0 NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REPERENCE/DOCKET UNBER: 01017/32953
TELECOMPUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEPRAK: 312/474-0448 Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS: ; TOPOLOGY: linear; ; MOLECULE TYPE: protein; ; SEQUENCE DESCRIPTION: SEQ ID NO: 61: US-09-604-325A-61 Sequence 61, Application US/09604325A Patent No. 6852313 GENERAL INFORMATION: APPLICANT: Zsebo, Krisztina M. INFORMATION FOR SEQ ID NO: 61: SEQUENCE CHARACTERISTICS: LENGTH: 273 amino TYPE: amino acid 19 121 121 Query Match ð

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241 QPSLTRAVENIQINEEDNBISMLQEKEREFQEV 273

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Search completed: February 22, 2006, 18:21:59 Job time : 34.0909 secs

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NAME: Clough, David W. REGISTRATION NUMBER: 36,3 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-005-243-49
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1 MKKTQTWILTCIYLQLLLFN.....NBEDNEISMLQEKBREFQEV 273
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(cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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Biocceleration Ltd.
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US-09-224-683-49
US-09-224-683-49
US-10-175-608-49
US-10-175-608-49
US-10-620-642-61
US-10-175-608-48
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US-09-224-683-50
US-09-224-683-50
US-09-224-683-50
US-09-224-683-50
US-09-224-683-63
US-09-224-683-50
US-09-224-683-63
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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No.
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Sequence 42, A
Sequence 55, A
Sequence 55, A
Sequence 4, Ap
Sequence 55, A
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Sequence
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Sequence
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COUNTRY: United States of America ZIP: 61066-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: PatentIn Release #1.0, Version #1.30

CURRATING SYSTEM: PC-DOS/MS-DOS CURRATING SYSTEM: PC-DOS/MS-DOS PERLICATION NUMBER: US/09/005,243
ALIGNMENTS
                                                                                                                                                                                                                                                                                                            Sequence 49, Application US/09005243
Patent No. US20020018763A1
GENERAL INPORMATION:
APPLICANT: Zeebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIPTCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIPTCATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 07/59,701
PRIOR APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION NUMBER: 07/573,616
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGANT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 240
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; Sequence 61, Application US/09005243
; Patent No. US2020201876341
; GENERAL INFORMATION:
    APPLICANT: Zeebo, Krisztina M.
    APPLICANT: Bosselman, Robert A.
    APPLICANT: Buggs, Sidney V.
    APPLICANT: Martin, Francis H.
    CORRESPENDENCE ADDRESS:
    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 61300 Sears Tower, 233 South Wacker Drive CITY: Chicago
    STATE: Illinois Cars Tower, 233 South Wacker Drive CUNTRY: United States of America
    COUNTRY: United States of America
    CONPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM FC compatible
    OMPUTER: IBM FC compatible
    OMPUTER: IBM FC compatible
    OMPUTER: BALEIN RELEASING SYSTEM: RC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/005,243
                                                                                                                                                                                                                                                                                                                                                        DB 3; Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 1397; DB 3; Best Local Similarity 100.0%; Pred. No. 8.5e-122; Matches 273; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 QPSLTRAVENIQINEEDNEISMLQEKEREFGEV 273
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEPAX: 312/474-0448
TELEX: 25-3856
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-09-005-243-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-005-243-61
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVINNVKDVTKLVANLFKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 MDVLPSHCWISEWVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-224-881-49.
US-09-224-881-89.
US-09-224-881-89.
US-0020031491A1
GENERAL INFORMATION:
APPLICANT: Zeseo, Kristina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Buggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCES: 104
CORRESPONDENCES: Marball, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CULTY: Chicago
STREET: 111inois
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 OPSLIRAVENIQINEEDNEISMLQEKEREPQEV 273
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                                                                                                                                                                                                                                                                                                                                                                                                               01017/34465
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-0CT-1990
PRIOR APPLICATION DATA:
APPLICATION UNBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-0CT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 31017/34
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 273 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-09-005-243-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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US-09-224-683-49
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GENERAL INCORANTION
GENERAL INCORANTION
GENERAL INCORANTION
APPLICANT: Boseslann, Robert A. AP
                                Sequence 61, Application US/09224683 Patent No. US20020031491A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 273 amino acids
amino acid
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Matches 273; Conservative
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MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKKTQTWILTCIYLQLLLENPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
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Best Local Similarity 100.0%; Pred. No. 8.5e-122;
Matches 273; Conservative 0; Mismatches 0; Indels 0
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE: US/09/224,683
FILING DATE: 12-JAN-1998
CLASSIFICATION: DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION: DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION: UNMBER: 08/49,653
FILING DATE: 25-NOV-1992
PRIOR APPLICATION NUMBER: 08/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION NUMBER: 01-OCT-1990
PRIOR APPLICATION NUMBER: 01-OCT-1990
PRIOR APPLICATION NUMBER: 01-OCT-1990
PRIOR APPLICATION NUMBER: 01-OCT-1989
FILING DATE: 11-JUN-1990
PRIOR APPLICATION NUMBER: 01017/35136
FILING PREERENCE/DOCKET NUMBER: 01017/35136
FILING PREERENCE/DOCKET NUMBER: 01017/35136
FILING PREERENCE/DOCKET NUMBER: 01017/35136
FILING PRIOR SEQ ID NO: 49: SEQUENCE CHARACTERISTICS:
LEBNGTH: 273 amino acids

NUMBER: 273 amino acids
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-49
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKRNSS 120
                                                                                                                                                                                                              9
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                                                                                                                                         1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
100.0%; Score 1397; DB 3; Length 273; 100.0%; Pred. No. 8.5e-122; Live 0; Mismatches 0; Indels 0
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US-09-224-683-61

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 240
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Masch, Kristina M.

Suggs, Sidney V.

Buggs, Sidney V.

Martin, Francis H.

TITLE OF INVENTION: Stem Cell Factor

NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: G300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STARE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER: READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/10/175,608

FILING DATE: 16-Oct-2002

CLASSIFTCATION NUMBER: 09/486,546

FILING DATE: 21-DEC-1993

APPLICATION NUMBER: 09/486,546

FILING DATE: 21-DEC-1993

APPLICATION NUMBER: 07/882,255

FILING DATE: 10-APW-1991

APPLICATION NUMBER: 07/882,255

FILING DATE: 10-APW-1991

APPLICATION NUMBER: 09/589,701

FILING DATE: 10-APW-1991

APPLICATION NUMBER: 09/589,701

FILING DATE: 10-APW-1991

APPLICATION NUMBER: 09/573,616
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                                                                                                                                                                                   Length 273;
                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                   Query Match 100.0%; Score 1397; DB 4; Best Local Similarity 100.0%; Pred. No. 8.5e-122; Matches 273; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPSLTRAVENIQINEEDNEISMLOEKEREFQEV 273
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECTLE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 61, Application US/10175608
Publication No. USZ0040181044A1
GENERAL INFORMATION:
APPLICANT: Zgebo, Krisztina M.
                                                                                                                 ;
US-10-175-608-49
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US-10-175-608-61
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                                                                                                           KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 240
                                                                                                                                                                                                                    MDALESHCWISEMVVQLSDSLTDLLDKFSNISECLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Geratein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago
STREET: 111inois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER: BADABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: BAPPE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: 10-Cct-2002
SOFTAME: PAPLICATION NUMBER: US/10/175,608
FILING DATE: 16-Cct-2002
RIGHG DATE: 24-MAY-1995
APPLICATION NUMBER: 09/635,249
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/982,255
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/684,535
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/684,535
FILING DATE: 10-CT-1991
APPLICATION NUMBER: 07/532,616
FILING DATE: 10-CT-1999
ATTORNEY/ABRAITON: NUMBER: 07/422,383
FILING DATE: 16-CCT-1999
ATTORNEY/ABRAITON NUMBER: 36,107
REGISTRATION NUMBER: 36,107
REGISTRATION NUMBER: 36,107
REGISTRATION NUMBER: 36,107
REGISTRATION NUMBER: 07/43-4380
TELLECOMMUNICATION INFORMATION:
NAME: Clough, David M.
REGISTRATION NUMBER: 36,107
REGISTRATION NUMBER: 30,107
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                             OPSLITRAVENIQINEEDNEISMLQEKEREFQEV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 49, Application US/10175608
Publication No. US20040181044A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
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SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
US-10-175-608-49
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61 MDVLPSHCWISEMVVQLSDSLIDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 KOLKKSPKSPEPRLFTPERFPRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKKTQTWILTCIYLQLLLENPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 1397; DB 5; Best Local Similarity 100.0%; Pred. No. 8.5e-122; Matches 273; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 OPSLTRAVENIQINEEDNEISMLOEKEREFORV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
                        APPLICATION DATA:
APPLICATION NUMBER: US/10/175,608
PILING DATE: 10-0ct-2002
APPLICATION NUMBER: 09/635,249
FILING DATE: 07-AUG-2000
APPLICATION NUMBER: 09/486,546
FILING DATE: 24-MAX-1995
APPLICATION NUMBER: 08/172,329
FILING DATE: 21-DC-1993
APPLICATION NUMBER: 07/684,535
FILING DATE: 25-NOV-1992
APPLICATION NUMBER: 07/684,535
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/53,616
FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/573,616
FILING DATE: 11-00-07-1991
APPLICATION NUMBER: 07/573,616
FILING DATE: 11-00-07-1990
APPLICATION NUMBER: 07/573,616
FILING DATE: 11-00-07-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-00-07-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 11-00-07-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-620-642-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 61, Application US/10620642; Publication No. US20050080250A1; CENERAL INFORMATION: APPLICANT: Seebo, Krisztina M. Bosselman, Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: «Unknown»
INFORWATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
US-10-620-642-61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKKIQIWILICIYLQLLLENPLVKIEGICRNRVINNVKDVIKLVANLPKOYMITLKYVPG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MDVLPSHCWISEMVVQLSDSLTDLLDKPSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
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STATE: 111nois
COUNTRY: United States of America
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 1397; DB 4; Best Local Similarity 100.0%; Pred. No. 8.5e-122; Matches 273; Conservative 0; Mismatches 0;
                                                                                                                                        NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPAK: 312/474-6300
TELEPAK: 312/474-0448
TELEPAK: 312/474-0448
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYRE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
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Publication No. US20050080250A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/10/620,642
FILING DATE: 16-Jul-2003
                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 61:
                                            FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INPORMATION:
FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/537,198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
US-10-620-642-49
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(US-09-005-243-48

) Sequence 48, Application US/09005243

) Farent No. US20020018763A1

) Farent No. US20020018763A1

) GENERAL INFORMATION:

APPLICANT: Sugge, Krisztina M.

APPLICANT: Sugge, Sidney V.

APPLICANT: Martin, Francis H.

) TITLE OF INVENTION: Stem Cell Factor

NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESS:

ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STREET: 111inois

COUNTRY: United States of America

ZIP: 6060-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC COMPATA:

APPLICATION NUMBER: US/09/005,243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1392; DB 3; Length 273; Pred. No. 2.5e-121;
                                                                                                                                            241 QPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
                                                                                                               241 OPSLIRAVENIQINEEDNEISMLOEKEREFOEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, DATA:
REGISTRATION NUMBER: 36,107
REGISTRATION NUMBER: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 312/*.
TELEFAX: 312/*.
TELEK: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
"VDR: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.6%;
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MOLECULE TYPE: protein
US-09-005-243-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
CITY: Chicago
STATE: 111inois
COUNTRY: United States of America
ZIP: 66066-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 1397; DB 5; Length 273; Best Local Similarity 100.0%; Pred. No. 8.5e-122; Matches 273; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEB PC compatible
CORPUTER: IEB PC compatible
CORPUTER: IEB PC compatible
CORPUTER: IEB PC compatible
CORPUTER: IEB PC compatible
CURRENT APPLICATION NUMBER: US/10/620,642
FILING DATE: 16-Jul-2003
CLASSIFICATION NUMBER: US/10/175,608
FILING DATE: 16-CL-2003
APPLICATION NUMBER: 09/635,249
FILING DATE: 07-AUG-2000
APPLICATION NUMBER: 09/486,546
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 09/172,329
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 09/68,701
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 09/589,701
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 09/589,701
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 09/589,701
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 09/537,198
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/573,616
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/42,383
FILING DATE: 14-4-6100
TELERPOMENATION NUMBER: 07/4-6100
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 61:
US-10-620-642-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acid
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKKTQTWILTCIYLQLLLENPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWPAMALPALFSLIGFAFGALYWKKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKKTQTWILTCIYLQLLLPNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREFT: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: 111inois COUNTRY: United States of America ZIP: 6606-6402
COUNTRY: Washabar FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 273;
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COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOOTWARE: Patentin Release #1.0, Version #1.30
CURRNT APPLICATION DATA:
APPLICATION NUMBER: US/10/175,608
FILING DATE: 16-Oct-2002
CLASSIFICATION: <UNknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/635,249
FILING DATE: 07-A002-2000
FILING DATE: 07-A002-2000
APPLICATION NUMBER: 09/486,546
FILING DATE: 24-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 99.6%; Score 1392; DB 3; Best Local Similarity 99.6%; Pred. No. 2.5e-121; Matches 272; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
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Publication No. US20040181044A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                     01017/35136
                                                                            REFERENCE/DOCKET NUMBER: 0101
TELECOMMUNICATION INFORMATION:
TELERANS: 312/474-6500
TELERA: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: 110ear
                                                        36,107
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,3
                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-09-224-683-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-175-608-48
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                                                                                                                                                              MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                           61 MDVLPSHCWISEMVVQLSDSLTDLLDKPSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                          KOLKKSPKSPEPRLFTPEEPFRIFNRSIDAFKDPVVASETSDCVVSSTLSPEKDSRVSVT 180
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                                                                                     1 MKKIQIWILICIYLQLLLENPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                     1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                            121 KDLKKSFKSPERPRLFTPEEFPRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT
                                                                                                                                                                                                                                                                                                                                                                                   181 KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
APPLICANT: Martin, Francis H.
APPLICANT: Martin, Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
  1; Indels
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APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION NUMBER: US/09/224,683
FILING DATE:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION NUMBER: 07/982,255
FILING DATE: 25-MOV-1992
PRIOR APPLICATION NUMBER: 07/589,701
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 12-MOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/53,616
FILING DATE: 24-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/53,616
FILING DATE: 12-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/53,198
FILING DATE: 11-MAY-1990
PRIOR APPLICATION NUMBER: 07/53,198
FILING DATE: 11-MAY-1990
PRIOR APPLICATION NUMBER: 07/53,198
PRIOR APPLICATION NUMBER: 07/53,198
PRILING DATE: 11-MAY-1990
PRIOR APPLICATION NUMBER: 07/53,198
PRILING DATE: 11-MAY-1990
PRILING DATE: 11-MAY-1990
PRILING DATE: 11-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 QPSLTRAVENIQINEEDNEISMLQEKEREFGEV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 QPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Marshall, O'Toole, Gerste STREET: 6300 Sears Tower, 233 South CITY: Chicago STATE: 1111nois SCOUNTRY: United States of America ZIP: 60606-6402 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
PILING DATE: 16-0CT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 48, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
272; Conservative
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                                                                                                                                                              19
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Matches
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TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-10-620-642-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 312/474-0448
TELEX: «Unknown»
INFORWATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
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ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: 111inois COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 99.6%; Score 1392; DB 4; Length 273; Best Local Similarity 99.6%; Pred. No. 2.5e-121; Matches 272; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                              NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELERX: 401Anom>
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
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Publication No. US20050080250A1

GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
APPLICATION NUMBER: 08/172,329
FILING DATE: 21-DEC-1933
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
APPLICATION NUMBER: 07/684,535
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/573,616
FILING DATE: 10-OCT-1991
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-UUN-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             | LENGTH: 273 amino acids | TYPE: amino acids | TYPE: amino acid | TOPOLOGY: linear | TOPOLOGY: linear | SEQUENCE DESCRIPTION: SEQ ID NO: 48: US-10-175-608-48
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US-10-620-642-48
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121 KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
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COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
CURRENT APPLICATION NUMBER: US/10/620,642
FILING DATE: 16-Jul-2003
CLASSIFICATION NUMBER: US/10/175,608
FILING DATE: 16-Jul-2003
APPLICATION NUMBER: 09/635,249
FILING DATE: 07-AUG-2000
APPLICATION NUMBER: 09/635,249
FILING DATE: 21-DE-1993
APPLICATION NUMBER: 09/172,329
FILING DATE: 21-DE-1993
APPLICATION NUMBER: 09/80,701
FILING DATE: 25-NOV-1992
APPLICATION NUMBER: 09/80,701
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 09/509,701
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 09/509,701
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 09/509,701
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 09/50,303
APPLICATION NUMBER: 09/50,303
APPLICATION NUMBER: 09/50,406
APPLICATION NUMBER: 07/573,616
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/50,303
APPLICATION NUMBER: 07/50,303
APPLICATION NUMBER: 07/422,383
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W:
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELERPHONE: 312/4/4-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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181 KPFMLPPVAASSLRNDSSSSNRKAKNPTGDSSLHWAAMALPAFPSLIIGFAFGALYWKKR 240
                                                                                                                                                              181 KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 240
61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 50, Application US/09224683

| Sequence 50, Application US/09224683
| Sequence 50, Application US/09224683
| Paten No. USZ0020031491A1
| GANRAL INFORMATION:
| APPLICANT: Seaselman, Robert A. APPLICANT: Buggs, Sidney V. APPLICANT: Suggs, Sidney V. APPLICANT: Wartin, Francis H. Information: Sea Cell Factor: Composition Claims Concressors Naturally o'Toole, Geratein, Murray & Borun STREET: G300 Sears Tower, 233 South Wacker Drive COUNTRY: Chicago STREE Marchall, O'Toole, Geratein, Murray & Borun STREET: Chicago STREE: Ploppy disk Computer: Concressors Natural Country: Chicago STREE: Ploppy disk COMPUTER: INFO Compatible COMPUTER: INFO Compatible COMPUTER: INFO COMPUTER: INFO COMPUTER: Barball Floppy disk CALSSIFICATION BATR: Barball Floppy disk CALSSIFICATION BATR: Barball Floppy disk Computer: Barb
                                                                                                                                                                                                                                                                           241 OPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
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US-09-224-683-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTXLVANLPKDYMITLKYVPG 60
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                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Marchall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chloago STATE: 11linois COUNTRY: United States of America ZIP: 60606-6402 CONPUTER READABLE FORM: MEDIUM TYPE: Eloppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentln Release #1.0, Version #1.30 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/005,243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 98.9%; Score 1381; DB 3; Length 273; Best Local Similarity 98.9%; Pred. No. 2.7e-120; Matches 270; Conservative 0; Mismatches 3; Indels
                                           Sequence 50, Application US/09005243
; Patent No. US2002001018731
; GENERAL INFORMATION:
APPLICANT: Zeabo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Bosselman, Robert A.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01017/34465
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FILING DATE:
RAPPLICATION NUMBER: 08/449,653
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
FILING APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-0CT-1990
PRIOR APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION NUMBER: 07/573,198
FILING DATE: 11-UUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-UUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-UUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-UUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Clough, David W. REGISTRATION NUMBER: 36,107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 01
TELECOMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
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linear
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MOLECULE TYPE: protein
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                 US-09-005-243-50
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STREET: 6300 Sears Tower, 233 South Wacker Drive
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                                                                                                                                                                                                                98.9%; Score 1381; DB 3; Length 273; 98.9%; Pred. No. 2.7e-120; ive 0; Mismatches 3; Indels
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STATE: Illinois
COUNTRY: United States of America
COUNTRY: United States of America
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/175,608
FILING DATE: 16-Oct-2002
CLASSIFICATION: CURNOWN>
PRIOR APPLICATION: AURHOWN>
PRIOR APPLICATION DATE:
CLASSIFICATION: AURHOWN>
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US-10-175-608-50
Sequence 50, Application US/10175608
Sequence 50, Application US/10175608
CENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION UNMERS: 09/635, 249
FILING DATE: 07-AUG-2000
PILING DATE: 07-AUG-2000
APPLICATION NUMBER: 09/486, 546
FILING DATE: 24-MAX-1995
APPLICATION NUMBER: 08/172, 329
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/684, 535
FILING DATE: 25-NOV-1992
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/684, 535
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 09/589, 701
INFORMATION FOR SEQ ID NO: 50
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                      Best Local Similarity 98.9
Matches 270; Conservative
                                                                                                                                                   ; MOLECULE TY
US-09-224-683-50
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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AFILING DATE: 10-CI-123,

APPLICATION NUMBER: 07/573,616

FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/537,198

FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/422,383
ATORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION NUMBER: 01017/35199
TELEPHONE: 312/474-0448
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

98.9%; Score 1381; DB 4;
Best Local Similarity 98.9%; Pred. No. 2.7e-120;
Matches 270; Conservative 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear;
HOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-10-175-608-50
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Sequence Seq

5224, 528, 5330, 5331, 534, 505, 505, 511, 511, 511,

Scoring table:

Minimum DB Maximum DB

Database

Perfect score:

Sequence:

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Run

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RESULT 1

19-10-353-783-49

19-10-353-783-49

19-10-353-783-49

19-10-353-183-183

19-10-351-180-0. USCO05261175A1

19-10-351-180-0. USCO05261175A1

19-10-351-180-0. USCO05261175A1

19-10-351-180-0. USCO05261175A1

19-10-360-351-180-0. USCO05261175A1

19-10-360-351-180-0. USCO05261175A1

19-10-360-361-0. USCO05261175A1

19-10-361-0. USCO05261

19-10-361-0. USCO0
US-11-176-830-512
US-11-176-830-514
US-11-176-830-518
US-11-176-830-524
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US-11-176-830-534
US-11-176-830-542
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US-11-176-830-507
US-11-176-830-507
US-11-176-830-511
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       ; Search time 10.5289 Seconds (without alignments) 386.005 Million cell updates/sec
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1397
1 MKKTQTWILTCIYLQLLLFN......NBEDNBISMLQBKBREFQBV
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1: /cgnZ 6/ptodata/2/pubpaa/USO6 NEW PUB.pep:*
2: /cgnZ -6/ptodata/2/pubpaa/USO6 NEW PUB.pep:*
3: /cgnZ 6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*
4: /cgnZ 6/ptodata/2/pubpaa/PCT_NEW PUB.pep:*
5: /cgnZ 6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*
6: /cgnZ 6/ptodata/2/pubpaa/USO0 NEW PUB.pep:*
7: /cgnZ 6/ptodata/2/pubpaa/USI0_NEW_PUB.pep:*
8: /cgnZ 6/ptodata/2/pubpaa/USI1_NEW_PUB.pep:*
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Biocceleration Ltd.
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US-10-353-783-61
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US-11-176-830-206
US-11-176-830-519
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                               version 5
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Maximum Match 100%
Listing first 45 summaries
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                            GenCore
Copyright (c) 1993
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seq length: 200000000
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Result

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RESULT 3
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                                                                                                                                                                                                                                                                                                                                            MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                                                                                                                                                                                                                          Gaps
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Sequence 61, Application US/10353783

Publication No. US20050261175A1

GENERAL INFORMATION:

BOSSELMAN, Robert A.

Suggs, Sidney V.

MARTIN, Francis H.

TITLE OF INVENTION: Seem Cell Factor

NUMBER OF SEQUENCES: 104

CORRESPONDENCES: 104

CORRESPONDENCES: 105

CORRESPONDENCES: 106

CORRESPONDENCES: 107

CITY: Chicago

STREET: 6300 Sears Tower, 233 South Wacker Drive

COUNTRY: United States of America

STREET: Illinois

COUNTRY: United States of America

STREET: Illinois

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: PROPABLE FLORM:

MEDIUM TYPE: Floppy disk

CORPUTER: PROPABLE FLORM:

MEDIUM TYPE: ROMAN-DOS

SOFTWARR: PATENTION NUMBER: US/10/353,783

FILING DATE: 28-Jan-2003

CURRENT APPLICATION NUMBER: US/10/353,783

FILING DATE: 28-Jan-2003
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                                                                                                                                                                                                                                                                  100.0%; Score 1397; DB 6; Length 273; 100.0%; Pred. No. 8.2e-118; tive 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/448,729
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 06/172,329
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
STRANDEDNESS: single
TOPOLCGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-353-783-49
TELECOMMUNICATION INFORMATION
                                         INPORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
             TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 273; Conservative
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US-10-353-783-61
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181 KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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APPLICANT Zeebo, Krisztina M.
Bosselman, Robert A.
Suggs, Sidney V.
Suggs, Sidney V.
Martin, Francis H.

TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Geratein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Childoole
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER: Elappy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 1397; DB 6; Best Local Similarity 100.0%; Pred. No. 8.2e-118; Matches 273; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                          ATTORNEY/AGENT INPORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32958A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 QPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
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FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-UN-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 61:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIGFAFGALYWKKR 240
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                                                                      ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                               CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
COUNTRY: United States of America
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ish PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/353,783
FILING DATE: 28-Jan-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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98.9%; Pred. No. 2.2e-116;
iive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01017/32958A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 25-NOV-1992
APPLICATION NUMBER: 07/684,535
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-ANG-1990
APPLICATION NUMBER: 07/573,616
TITLE OF INVENTION: Stem Cell Factor NUMBER OF SEQUENCES: 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/448,729
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 08/172,329
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/982,255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 010
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 273 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
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                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: <Unknown>
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Best Local Similarity 98.9
Matches 270; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KOLKKSPKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
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  Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 99.6%; Score 1392; DB 6; Best Local Similarity 99.6%; Pred. No. 2.3e-117; Matches 272; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 01017/32958A TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
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                                                                                                                                                                                                             FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
APPLICATION NUMBER: 07/684,535
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/689,701
FILING DATE: 01-OCT-1990
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/57,198
FILING DATE: 11-UIN-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 11-CCT-1989
ATTORNEY/AGENT INFORMATION:
NAMB: Clough, David W.
REGISTRATION NUMBER: 36,107
                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/353,783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; ; MOLECULE TYPE: protein; ; SEQUENCE DESCRIPTION: SEQ ID NO: 48: US-10-353-783-48
                                                                                                                                      APPLICATION NUMBER: 08/448,729
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 08/172,329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 50, Application US/10353783
Publication No. US20050261175A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
Bosselman, Robert A.
Suggs, Sidney V.
                                                                    FILING DATE: 28-Jan-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 312/474-6300
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: <Unknown>
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US-10-353-783-50
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APPLICANT: Gantier, Rene
APPLICANT: Gantier, Rene
APPLICANT: Given, Thierry
APPLICANT: Given, Thierry
APPLICANT: Given, Thierry
APPLICANT: Ustranti, Lila
APPLICANT: Vega, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nur
TITLE OF INVENTION: Acid Molecules and Related Applications
TITLE OF INVENTION: Acid Molecules and Related Applications
TITLE OF INVENTION: UNMER: US/11/176, 830
CURRENT APPLICATION NUMBER: US/11/176, 830
CURRENT FILING DATE: 2003-09-08
PRIOR FILING DATE: 2003-09-08
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-09-09
NUMBER: OF 40409, 898
PRIOR FILING DATE: 2002-09-09
NUMBER: OF 501 D NOS: 1306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
90.6%; Score 1265; DB 7; L
Best Local Similarity 100.0%; Pred. No. 4.7e-106;
Matches 248; Conservative 0; Mismatches 0;
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Pred. No. 7e-106;
PRIOR APPLICATION NUMBER: 10/658, 934
PRIOR FILING DATE: 2003-09-08
PRIOR FILING DATE: 2003-09-08
PRIOR FILING DATE: 2003-03-21
PRIOR FILING DATE: 2002-09
NUMBER OF SEQ ID NOS: 1306
SEQ ID NO 206
                                                                                                                                                                                                                                                                                                                                                                                                                             PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank AAA85450
DATABASE ENTRY DATE: 1996-01-19
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                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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US-11-176-830-520
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Best Local Similarity
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SEQ ID NO 520
LENGTH: 248
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Best Local
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Publication No. US20060008872A1

GENERAL INFORMATION:
APPLICANT: MEDEXCEN Inc.
APPLICANT: CHUNG, Youg-Hoon
APPLICANT: LEE, Hak-sup
APPLICANT: YI, Ki-wan
APPLICANT: HEO, Youn-Hwa
TITLE OF INVENTION: A method of improving efficacy of biological response-modifying
TITLE OF INVENTION: A method of improving efficacy of biological response-modifying
TITLE OF INVENTION: Droteins and the example muteins
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/519,390
CURRENT APPLICATION NUMBER: KR10-2003-0051846
PRIOR FILING DATE: 2004-12-23
PRIOR FILING DATE: 2003-07-26
NUMBER OF SEQ ID NOS: 65
SEQ ID NO 24
LENGTH: 248
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Sequence 206, Application US/11176830

Sequence 206, Application No. USCO060020116A1

GENERAL INFORMATION:

APPLICANT: Gantier, Rene

APPLICANT: Guyon, Thierry

APPLICANT: Dritanti, Lila

APPLICANT: Vega, Manuel

TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding North Common Processing Common Processi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: SCF: 63rd, 102nd, 110th, 115th, 116th, 119th, 129th, 109th, 109th, 109th, 109th, 207th or 245th Phe is replaced by Val. US-10-519-390-24
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                                                     241 QPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
              241 OPSLTRAVENIQINEEDNEISMLOEKEREFOEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 248; Conservative
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KEREFOEV 248
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US-11-176-830-519

Sequence 519, Application US/11176830

Publication No. US20060020116A1

GENERAL INFORMATION:
APPLICANT: Gantier, Rene
APPLICANT: Gayon, Thierry
APPLICANT: Use, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding William APPLICANT: Vega, Manuel
TITLE OP INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Wilter Brererence: 17109-012002 (9228)
CURRENT APPLICATION NUMBER: US/11/176,830
CURRENT APPLICATION NUMBER: 06/457,135
FRIOR APPLICATION NUMBER: 66/457,135
FRIOR PILING DATE: 2003-09-09
FRIOR FILING DATE: 2003-09-09
FRIOR FILING DATE: 2002-09-09
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APPLICANT: Gantier, Rene
APPLICANT: Gayon, Thierry
APPLICANT: Gayon, Thierry
APPLICANT: Drittenti, Lila
APPLICANT: Drittenti, Lila
APPLICANT: Vega, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
TITLE OF INVENTION: Acid Molecules and Related Applications
TITLE OF INVENTION: 17109-012002 (9228)
CURRENT APPLICATION NUMBER: US/11/176,830
CURRENT FILING DATE: 2005-07-06
PRIOR FILING DATE: 2003-09-08
PRIOR FILING DATE: 2003-09-08
PRIOR APPLICATION NUMBER: 60/457,135
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Pred. No. 8.6e-106;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.6%;
Matches 247; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-176-830-519
   241 KEREFOEV 248
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| Sequence 537, Application US/11176830
| Publication No. US2006020116A1
| GENERAL INFORMATION:
| APPLICANT: Gantier: Rene
| APPLICANT: Usery
| AUTHE OF INVENTION: Acid Molecules and Related Applications
| FILE OF INVENTION: Acid Molecules and Related Applications
| FILE OF INVENTION: Acid Molecules and Related Applications
| FILE OF INVENTION: Acid Molecules and Related Applications
| FILE OF INVENTION: Acid Molecules and Related Applications
| FILE OF INVENTION: Acid Molecules and Related Applications
| FILE OF INVENTION: Acid Molecules and Related Applications
| FILE OF INVENTION: Acid Molecules and Related Applications
| FILE OF PRIOR PELICATION NUMBER: 60/457,135 |
| PRIOR PELICATION NUMBER: 60/409,898 |
| PRIOR PELING DATE: 2003-09-09 |
| NUMBER OF SEQ ID NOS: 1306 |
| SEQ ID NO 537 |
| LENGTH: 248 |
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                                                                                            1 EGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPGMDVLPSHCWISEMVVQLSDSLTDLL 60
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   0; Indels
1; Mismatches
247; Conservative
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; ORGANISM: Homo sapiens
US-11-176-830-537
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US-11-176-830-537
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APPLICANT: Gantier, Rene
APPLICANT: Gantier, Rene
APPLICANT: Guyon, Thierry
APPLICANT: Guyon, Thierry
APPLICANT: Dittenti, Lila
APPLICANT: Dittenti, Lila
APPLICANT: Usea, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu;
TITLE OF INVENTION: Acid Molecules and Related Applications
FILE REFERENCE: 17109-012002 (9228)
CURRENT APPLICATION NUMBER: US/11/176,830
CURRENT APPLICATION NUMBER: 10/658,834
FRIOR APPLICATION NUMBER: 60/457,135
FRIOR APPLICATION NUMBER: 60/457,135
FRIOR FILING DATE: 2003-09-09
FRIOR FILING DATE: 2003-09-09
FRIOR FILING DATE: 2002-09-09
NUMBER: OF SEQ ID NOS: 1306
SEQ ID NO 538
SEQ ID NO 538
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; Sequence 499, Application US/11176830
; Publication No. US20060020116A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 538, Application US/11176830; Publication No. US20060020116A1; GENERAL INFORMATION:
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Matches 247; Conservative
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Publication No. US20060020116A1

GENERAL INFORMATION:

APPLICANT: Gauyon, Thierry

APPLICANT: Gauyon, Thierry

APPLICANT: Gayon, Thierry

APPLICANT: With a price of the price
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Pred. No. 8.6e-106;
1; Mismatches 0;
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90.3%; Score 1262; DB 7;
Best Local Similarity 99.6%; Pred. No. 8.6e-106;
Matches 247; Conservative 1; Mismatches 0;
  PRIOR FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: 60/409,898
PRIOR FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: PASLSEQ for Windows Version
SEQ ID NO 529
LENGTH: 248
                                                                                                                                                                                                                                                                                                     90.3%;
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Best Local Similarity 99.6
Matches 247; Conservative
                                                                                                                                                                                         TYPE: PRT
CORGANISM: Homo sapiens
US:11-176-830-529
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US-11-176-830-536
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US-11-176-830-536
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APPLICANT: Gantier, Rene
APPLICANT: Gantier, Rene
APPLICANT: Gantier, Rene
APPLICANT: Gantier, Rene
APPLICANT: Gantier, Inla
APPLICANT: Usupon, Thierry
APPLICANT: Usupon, Thierry
APPLICANT: Vega, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nh
TITLE OF INVENTION: 17109-012002 (922B)
CURRENT APPLICATION NUMBER: 10/658,834
FILE REFERENCE: 11109 DATE: 2005-07-06
PRIOR FILING DATE: 2003-09-08
PRIOR APPLICATION NUMBER: 60/457,135
PRIOR APPLICATION NUMBER: 60/457,135
PRIOR FILING DATE: 2003-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: FREISEQ for Windows Version 4.0
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                                                                                           90.3%; Score 1261; DB 7;
99.6%; Pred. No. 1.1e-105;
tive 1; Mismatches 0;
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Best Local Similarity 99.6%; Pred. No. 1.1e-105;
Matches 247; Conservative 1; Mismatches 0;
                                                                                                                                                                                                              Sequence 501, Application US/11176830 Publication No. US20060020116A1
                                                                                        Query Match
Best Local Similarity 99.61
Matches 247; Conservative
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-176-830-500
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US-11-176-830-501
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Sequence 500, Application US/11176830

Publication No. US20060020116A1

GENERAL INFORMATION:
APPLICANT: Guyon, Thierry
APPLICANT: Guyon, Thierry
APPLICANT: Drittenti, Lila
APPLICANT: Vega, Manuell Evolution of Cytokines for Higher Stability, Encoding Nu TITLE OF INVENTION: Actional Evolution of Cytokines for Higher Stability, Encoding Nu TITLE OF INVENTION: Actional Evolution of Cytokines for Higher Stability, Encoding Nu TITLE OF INVENTION NUMBER: US/11/176,830

CURRENT APPLICATION NUMBER: 10/58,834

PRIOR APPLICATION NUMBER: 60/457,135

PRIOR PILING DATE: 2003-09-08

PRIOR PILING DATE: 2003-09-08

PRIOR FILING DATE: 2002-09-09

NUMBER OF SEQ ID NOS: 1306

SEQ ID NO 500

LENGTH: 248
       APPLICANT: Gartier, Rene
APPLICANT: Gartier, Rene
APPLICANT: Gartier, Lila
APPLICANT: Guyon, Thierry
APPLICANT: Drittanti, Lila
APPLICANT: Drittanti, Lila
APPLICANT: Vega, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
TITLE OF INVENTION: Rational Evolution Solution Number: 10/658,834
PRIOR PILING DATE: 2003-09-08
PRIOR PILING DATE: 2003-09-08
PRIOR FILING DATE: 2003-09-09
NUMBER OF SEQ ID NOS: 1306
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90.3%; Score 1261; DB 7;
Best Local Similarity 99.6%; Pred. No. 1.1e-105;
Matches 247; Conservative 1; Mismatches 0;
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US-11-176-830-499
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New naturally-occurring polypeptide stem cell factor analogues - have haematopoietic biological activity of stem cell factor and are used to treat e.g. leukopenia, AIDS, nerve damage and infertility.
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90US-00537198.
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Zsebo KM, Suggs SV,
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N-PSDB; AAQ11543.
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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 germ stem cells. The
stem cells such as neural stem cells and primordial germ stem cells. The product may be used in a pharmaceutical compsn. for treating, in a mammal, leukopenia, thrombocytopenia, nanemia, AIDS, neoplasia, nerve damage, infertility and intestinal damage. See also AAR11/08, AAQ11509-
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100.0%; Pred. No. 3e-121;
ive 0; Mismatches 0
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/label=_sig_peptide
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/label= mat_SCF
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90US-00537198.
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Best Local Similarity 100.
Matches 245; Conservative
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15-MAY-1996
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carcinoma cell line. Non-naturally occuring SCF and C-terminally carcinoma cell line. Non-naturally occuring SCF and C-terminally curring SCF stimulate growth of printitive funciative of naturally occuring SCF stimulate growth of printitive progenitors such as haemaclopicatic progenitor cells, neural stem cells and primordial germ stem cells. The peptides can be used in a composition of contracting leucopenia, anaemia or thrombocycopenia, for enhancing engrathment of bone marrow during transplantation or for bone marrow recovery after chemotherapy or radiation-induced bone marrow aplasia or myelosuppression. They can also be used for treating neoplasia, nerve damage, infertlilty, intestinal damage or myelosupoliferative disorders. Antibodies may be raised against the peptides for use in detection or house and severe combined immunodeficiency (SCID) states alone or in combination with other factors such as IL-7. (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                    AAR83979 is a human stem cell factor (SCF) derived from the 5637 bladder
New stem cell factor polypeptide(s) - for stimulating the growth of primitive progenitor cells, esp. for treating disorders involving blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
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100.0%; Pred. No. 3e-121;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB98368 standard; protein; 245 AA
                                                                                                                                               Claim 9; Fig 44; 127pp; English.
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Matches 245; Conservative
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The present sequence representing human SCF (stem cell factor) protein is isolated from the 5637 bladder carcinoma cell line. The present invention crlates to novel stem cell factors (AAU02453, AAU02460) and the polymucleotides encoding them. SCF stimulate primitive progenitor cells including early haematopoietic progenitor cells. The invention also describes SCF peptides (AAU02462-AAU02481) and the oligonucleotides (AAS040117) used in the isolation of human and rat SCF sequences. The polymucleotide encoding SCF is useful for producing SCF and useful in compension of the sequences. The polymucleotide encoding SCF is useful for producing SCF and useful in compension in the isolation of human and rat SCF sequences. The polymucleotide encoding SCF is useful for treating disorders involving blood cells cuch as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple myeloma, Hoddxin's disease, lymphoma, Gaucher's disease, ansemia, congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis, disseminated fungus disease, Pulminating septicemia, malaria, vitamin B12 and folic acid deficiency, pyridoxine deficiency, and hypopigmentation construction and vitiligo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 KOLKKSFRSPEPRLFTPBEFFRIFMRSIDAFKDFVVASETSDCVVSSTLSPEKGKAKNPP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acids encoding stem cell factor useful for treating disorders involving blood cells, e.g. leukemia, splenomegaly, Hodgkin's disease, Kala azar, anemia and septicemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKKTQTWILICIYLQLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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  blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly; anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder; 5637 bladder carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 245;
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100.0%; Pred. No. 3e-121;
tive 0; Mismatches 0
                                                                                                                                1. .25 ......./label= Signal_peptide 26. .245
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                                                                                                                          Location/Qualifiers
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/label= Mature_SCF
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90US-00537198.
90US-00573616.
90US-00589701.
93US-00172329.
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MARTIN F H.
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01-OCT-1990;
21-DEC-1993;
                                                                                      Homo sapiens
                                                                                                                                                                                                                                                US6207417-B1
                                                                                                                                                                                                                                                                                                                                07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SUGG/)
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                                                                                                                              Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a method for enhancing (B) the efficiency of transfer of a polynucleotide (I) into a target mammalian cell (II) in vitro, comprising exposing (II) that expresses a stem cell factor (SCP) receptor to a biologically active SCP, its analogue or fragment, which induces cell proliferation, and introducing (I) to (II) in vitro. Exposure of SCF to (II) results in increased uptake of (I) into the cell. The method is useful for enhancing the efficiency of the transfer of a polynucleotide into a target mammalian cell in vitro. The method is useful in gene therapy techniques. Ad443301 to Ad443364 and AAB98351 to AAB98390 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KDLKKSPKSPBPRLFTPBBFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPBKGKAKNPP 180
                                                                                                                                                                                                                                                                                                                            Enhancing efficiency of transfer of polynucleotide into a target mammalian cell in vitro, involves exposing cell that expresses a stem cell factor receptor to stem cell factor, and introducing polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human SCF protein isolated from the 5637 bladder carcinoma cell line.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; stem cell factor; SCF; early haematopoietic progenitor cell;
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Pred. No. 3e-121;
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100.0%; Pred. No. sc
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 18; Fig 44; 210pp; English.
89US-00422383.
90US-00537198.
90US-00573616.
92US-00982255.
93US-00172329.
95US-00449653.
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Best Local Similarity
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                                          24-AUG-1990;
01-OCT-1990;
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01-OCT-1990;
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                                    The present invention provides the protein and coding sequences of mammalian stem cell factors (SCF8). These are capable of stimulating the growth of early haematopoietic progenitor cells, neural stem cells and primordial germ stem cells. The sequences are useful in the treatment of leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal neuroglobinuria, malaria, pigmentation disorders, neurological and intestinal damage, infertility, AIDS and severe combined immunodeficiency (SCID). The present sequence is an SCF described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated non-human mammalian stem cell factor polypeptide stimulating growth of early hematopoietic progenitor cells, useful for treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar, sarcoidosis.
                                                                                                                                                                                                                                                                                                                                                                Human; rat; mammal; stem cell factor; SCP; cell growth stimulation; gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia; neurological damage; intestinal damage; infertility; AIDS; SCID; severe combined immunodeficiency.
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Pred. No. 3e-121;
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/label= signal_peptide
26. .245
/label= mature_stem_cell_factor
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                                                                                                                                                                                                                                                                                                                                  Human stem cell factor SEQ ID NO: 63.
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90US-00537198.
90US-00573616.
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92US-00982255.
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100.0%;
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N-PSDB; AAF89105.
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Best Local Similarity
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                                                                                          EFQEV 245
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24-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1990;
25-NOV-1992;
                                                                                                                                                                                                                                                                                                13-JUL-2001
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                                                                                                                                                                                                                                                          AAB96953;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
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                                                              61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                             1 MKKTQTWILITCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLFKDYMITLKYVPG
                                                 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                 KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKOFVVASETSDCVVSSTLSPEKGKAKNPP
1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                Human, stem cell factor; SCF; early haematopoietic progenitor cell; blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly; anaemia; Kala azar; septicaemia; malaria; hypopigmentation disorder;
                                                                                                                                                                                                                                                                                                                                                       Human SCF protein isolated from the 5637 bladder carcinoma cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .25
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 10; Fig 44A-44C; 166pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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/label= Mature SCF
                                                                                                                                                                                                                                                                                     AAB73568 standard; protein; 245
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90US-00537198.
90US-00573616.
90US-00589701.
91US-00684535.
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                                                                                                                                                                                                                                                                                                                                                                                                                        5637 bladder carcinoma.
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isolated from the 5637 bladder carcinoma cell line. The present invention relates to novel stem cell factors (AAB73561-AAB73568, AAB73571-AAB73576) and the polymucleotides encoding them. SCF stimulate primitive progenitor cells including early haematopoietic progenitor cells. The invention also describes SCF peptides (AAB73578-AAB73597) and the oligonucleotides (AAH73895) used in the isolation of human and rat SCF sequences. The polymucleotide encoding SCF is useful for producing SCF and useful in gene therapy. It is useful for treating disorders involving blood cells such as welofibrosis, metastatic carcinoma, acute leukaemia, multiple myeloma, Rodgkin's disease, lymphoma, Gaucher's disease, anaemia, congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis, disseminated fungus disease, Pulminating septicaemia, malaria, vitamin hypopigmentation disorders such as piebaldism and vitiligo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, stem cell factor; SCF, early haematopoietic progenitor cell,
blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
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                                                                                                                                                                                                               100.0%; Score 1262; DB 4
100.0%; Pred. No. 3e-121;
tive 0; Mismatches 0
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/label= Signal_peptide
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/label= Mature SCF
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                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 245; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5637 bladder carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EFQEV 245
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                                                                                                                                                                                        Sequence 245 AA;
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11-JUN-1990;
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The present sequence representing human SCF (stem cell factor) protein is isolated from the 5637 bladder carcinoma cell line. The present invention relates to novel stem cell factors (AAU02761-AAU02776), AAU02770-AAU02775, AAU02779) and the polynuclectides encoding them. SCF stimulate primitive progenitor cells including early haematopoietic progenitor cells. The invention also describes SCF peptides (AAU02777-AAU02794) and the coligonuclectides (AAS04182-AAS04218) used in the isolation of human and rat SCF sequences. The polynuclectide encoding SCF is useful for rat SCF sequences. The polynuclectide encoding SCF is useful for treating disorders involving blood cells such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease.

Iymphoma, Gaucher's disease, anaemia, congestive splenomegaly, Kala azar, arcoidosis, military tuberculosis, disease, canaemia, them seminated fungus disease, rulminating septicemia, malaria, vitamin Bl2 and follc acid deficiency, pyridoxine deficiency, and hypopigmentation disorders such as piebaldism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 GDSSLHWAAMALPALFSLIGFAFGALYWKKRQPSLTRAVENIQINEEDNEISMLGEKER 240
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                                                                                                                                                                                                                                                                                                                                  Isolated DNA sequence, encoding polypeptide product useful for stimulating growth of early hematopoietic progenitor cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 1262; DB 4; Length 245; 100.0%; Pred. No. 3e-121; tive 0; Mismatches 0; Indels 0.
                                                                                                                                                                                 Martin FH;
                                                                                                                                                                                                                                                                                                                                                                                                                          Example 5; Fig 44A-44C; 167pp; English.
                                                                                                                                                                                    RA, Suggs SV,
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90US-00573616.
90US-00589701.
92US-00982255.
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Matches 245; Conservative
                                                                                                                                                                                 Zsebo KM, Bosselman
                                                                                                                                                                                                                                         WPI; 2001-281051/29.
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                                                                                                                    (AMGE-) AMGEN INC.
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24-AUG-1990;
01-OCT-1990;
25-NOV-1992;
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The present invention relates to novel non-naturally-occurring stem cell factor (SCF) polypeptides having an amino acid sequence sufficiently duplicative of that of naturally-occurring SCF to allow possession of hematopoietic biological activity of naturally occurring SCF. Sequences of the invention are useful for treating leucopaenia, thrombocytopaenia, anaemia and for enhancing bone marrow recovery in treatment of radiation, engraftment of bone marrow during transplantation in mammals and chemical or chemotherapeutic induced bone marrow aplasia or myeloeuppression. They are also useful for treating acquired immune deficiency in a human, nerve damage, noplasia, infertility, myeloproliferative disorder, intestinal damage in a mammal. SCF sequences are useful for preparing biologically active polymer polypeptide adduct, for enhancing transfection of early
181 GDSSLHWAAMALPALFSLIIGFAFGALYWKKRQPSLTRAVENIQINEEDNEISMLQEKER 240
                                                                                                                                                                                                                                                                                                                                                                                 Human; stem cell factor; SCF protein; leucopaenia; thrombocytopaenia; anaemia; myelosuppression; nerve damage; myelostoliferative disorder; infertility; neoplasia; myelofibrosis; myelosclerosis; osteopetrosis; metastatic carcinoma; acute leukaemia; multiple myeloma; sarcoidosis; hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease; Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar; Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopaenia; disseminated fungus disease; Pulminating septicaemia; piebaldism; AlDS; acquired immune deficiency syndrome; malaria; miltary tuberculosis; pyridoxine deficiency; vitamin Bl2 deficiency; folic acid deficiency; blamond Blackfan anaemia; hypopigmentation disorder; vitiligo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel non-naturally-occurring stem cell factor polypeptide, useful for treating leucopenia, thrombocytopenia, anemia and for enhancing engraftment of bone marrow during transplantation in a mammal.
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/label= Signal_peptide
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(BOSS/) BOSSELMAN R A.
(SUGG/) SUGGS S V.
(MART/) MARTIN F H.
                                                                                                                                                                                                                                                                                                                                            Human SCF protein #3
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                                               241 EPQEV 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents human stem cell factor (SCF). The cDNA encoding this sequence is isolated from the 5637 bladder carcinoma cell line. The sequence is described in an invention relating to novel stem cell factors, the polynucleotides encoding them and methods for producing the stem cell factors. The methods involve increasing the number of early haematopoietic progenitor cells in human peripheral blood by administering a hematopoietically effective human stem cell factor including myelofibrosis, myelosclerosis, osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma, Hodghin's disease, including myelofibrosis, sultiple myeloma, Hodghin's disease, humboma, Gaucher's disease, Niemann-Pick disease, refractory anaemia, malaria, vitamin B12 and folic acid deficiency, hypopigmentation disorders i.e. piebaldism and viral induced disorders, including AIDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Increasing the number of early hematopoietic progenitor cells in the peripheral blood useful for the treatment of blood disorders including Hodgkin's disease comprises the administration of human stem cell factor.
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                                                                                            1. .25
/label= Signal_peptide
26. .245
/label= Mature_SCF
                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Fig 44; 210pp; English.
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900S-00573616.
900S-00589701.
910S-00684535.
920S-00982255.
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                          Homo sapiens
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25-NOV-1992;
21-DEC-1993;
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haematopoietic progenitor cells with a gene, and transfer of a gene into a mammal. They are useful for treating myelofibrosis, myelosclerosis, osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-bick disease, Letterer-Sive disease, refractory erythroblastic anaemia, Di Guglielmo syndrome, congestive splenomegaly, Kala azar, sarcoidosis, primary splenic pancytopaenia, disseminated fungus disease, malaria, military tuberculosis, Phlminating septicaemia, pyridoxine deficiency, vitamin Bl2 and folic acid deficiency, Diamond Blackfan aneamia, hypopigmentation disorders such as piebaldism, AIDS (acquired immune deficiency syndrome) and vitiligo. The present sequence is human SCF protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 1262; DB 5; Length 245; 100.0%; Pred. No. 3e-121; Attive 0; Mismatches 0; Indels 0.
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90US-00537198.
90US-00573616.
90WO-US005548.
90US-00589701.
90EP-00310899.
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Best Local Similarity 100.
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11-JUN-1990;
24-AUG-1990;
01-OCT-1990;
04-OCT-1990;
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100.0%; Score 1262; DB 5; Length 245;
100.0%; Pred. No. 3e-121;
tive 0; Mismatches 0; Indels 0; Gaps 0;
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                                                                                                                                                                                                                         The present invention relates to novel stem cell factors (SCFB), polynucleotide sequences encoding the SCFB, and methods of producing them. SCFB are involved in the blood-forming (haematopoietic) system in mammals, particularly humans. The method of the invention is useful for the production of human SCP. The stem cell factors are useful to treat disorders involving blood cells e.g. metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, refractory erythroblastic anaemia, miliary tuberculosis, disseminated fungus disease, malaria, and vitiligo. The present sequence represents human SCF protein isolated from the 5637 bladder carcinoma cell line
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                                                                                                            Production of a human stem cell factor (SCF) polypeptide for treating disorders involving blood cells, such as leukemia, comprises culturing mammalian cells comprising non-human SCF promoter DNA linked to DNA
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                                Martin
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                                Bosselman RA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 245; Conservative
                                                                                                                                                                 encoding the human SCF.
                                Suggs SV,
                                                             WPI; 2002-684093/74.
N-PSDB; ABS73860.
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(AMGE-) AMGEN INC.
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                                Zsebo KM,
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ADP99333 standard; protein; 245 AA
ADP99333
            The invention relates to stem cell factor (SCF) polypeptides with ham the polymucleotides encoding them. The perpetides are used for treating infertility, intestinal danage, polypeptides are used for treating infertility, intestinal danage, myeloproliferative disorders, leuropenia, thrombocytopenia or anamia, for improving engraftment of bone marrow transplants, for enhancing bone marrow recovery after radiotherapy or chemotherapy and in treatment of immune deficiency, neoplasia, nerve danage, osteoporosis, metastatic carcinoma, leukaemia and miliary tuberculosis. The SCF polypeptides are also used to expand haematopoietic progenitor cells for transplantation on to prepare such cells for transfection with a gene. The SCF polymucleotides can be used for recombinant expression of the polymetides and also as probes for mapping of the SCF gene, for identifying SCF-related diseases and as a marker for neighbouring genes. Antibodies raised against the polymeptides are useful in diagnosis and to remove SCF from blood. This sequence represents an SCF polypeptide of the
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                                                                                                                                                                                                                                                                                                                                            New non-natural stem cell factor, useful for treating e.g. leucopenia or immune deficiency, also related nucleic acid and antibodies.
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                                                                                                                                                                                                                                                                      Suggs SV, Martin FH;
                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; SEQ ID NO 63; 217pp; English.
                                                        90US-00537198.
90US-00573616.
90US-00684501.
91US-00982255.
93US-00172329.
95US-00449653.
              98US-00224683
                                          89US-00422383
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Best Local Similarity 100.
Matches 245; Conservative
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                                                                                                                                                                                            (ZSEB/) ZSEBO K M.
(BOSS/) BOSSELMAN R A.
(SUGG/) SUGGS S V.
(MART/) MARTIN F H.
                                                                                                                                                                                                                                                                                                   WPI; 2003-851459/79.
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              31-DEC-1998;
                                                                                       01-OCT-1990
                                                                                                      10-APR-1991
25-NOV-1992
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12-JAN-1998
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RESULT

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Human; SCF; stem cell factor; gene therapy;
haematopoietic progenitor cell; aplastic anaemia;
haematopoietic progenitor cell; aplastic anaemia;
w paroxysmal nocturnal haemoglobinuria; myelofibrosis; myelosclerosis;
corresperzosis; metastatic carcinoma; acute leukaemia; multiple myeloma;
hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;
w Letterer-Siwe disease; refractory erythroblastic anaemia;
b) Guglielmo syndrome; congestive splenomegaly; Kala awar; sarcoidosis;
w primary splenic pancytopaenia; miliary tuberculosis;
primary splenic pancytopaenia; miliary tuberculosis;
w disseminated fungus disease; Pulminating septicaemia; malaria;
vitamin Bl2 deficiency; folic acid deficiency; pyridoxine deficiency;
biamond Blackfan anaemia; hypopigmentation disorder; piebaldism;
w ritiligo; neurological damage; infertility; intestinal damage;
irradiation; chemotherapy; ALDS; heematopoietic recovery;
acute blood loss; neoplasm; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to preparing a (vertebrate) human stem cell factor (SCF) polypeptide comprising growing host cells transformed or transfected with DNA encoding a human SCF that stimulates growth of haematopoietic progenitor cells under nutrient conditions, the DNA being operatively linked to an expression control sequence, and isolating the polypeptide produced. Also included is a recombinant host cell transfected with an expression construct comprising a vertebrate SCF polypeptide-encoding DNA operatively linked to a heterologous expression regulatory sequence, permitting the expression of the vertebrate SCF polypeptide in the host cell bisclosed as new are rat and human nucleic acids encoding SCF, SCF protein fragments. The DNA sequences are useful for effecting the large scale synthesis of SCF by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Preparing a human stem cell factor (SCF) polypeptide, useful for treating hematopoletic disorders, e.g., aplastic anemia, comprises growing host cells transformed or transfected with DNA encoding a human SCF.
                                                                                                                                    Human stem cell factor, SCF, protein (bladder cancer).
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    .25
    /note= "Signal peptide"

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90US-00537198.
90US-00587616.
91US-00587761.
91US-00684535.
92US-00172329.
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                                                                    23-SEP-2004 (first entry)
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24-AUG-1990;
01-OCT-1990;
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24-MAY-1995;
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25-NOV-1992
ADP99333;
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WO2004034995-A2 29-APR-2004.

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cc variety of recombinant techniques or for generating new and useful viral and circular plasmid DNA vectors, new and useful transformed and circular plasmid DNA vectors, new and useful transformed and transfected proKaryotic and eukaryotic host cells, and new and useful competed for cultured growth of such host cells, and new and useful competed for cultured growths. The second is several solutions of second is related products. The DNA sequences are also useful as competed probes in isolating human genomic DNA encoding SCF, in methods of protein synthesis, in genetic therapy in humans and other mammals, and competed solutions of second in developing transgenic mammalian species which may serve as eukaryotic in developing transgenic mammalian species which may serve as eukaryotic consetul for treating haematopoietic disorders, e.g., aplastic anaemia, consetul for treating haematopoietic disorders, e.g., aplastic anaemia, consecutors in metastatic carcinoma, acute leukaemia, multiple myeloma, contenter-Siw disease, lymphoma, Gaucher's disease, Niemann-Pick disease, Letterer-Siw disease, refractory erythroblastic anaemia, pick disease, congestive splenomegaly, Kala awar, sarcoidosis, primary splenic pancytopaenia, miliary tuberculosis, disseminated fungus disease, Confidentia, malaria, vitemin B 12 and folic acid deficiency, splenic pancytopaenia, malaria, vitemin B 12 and folic acid deficiency, pyridoxine deficiency, Diamond Blackfan anaemia, and hypopigmentation disorders such as piebaldiam and vitiligo. The SCF are also useful for treating neurological damage, infertility states, intestinal damage cresulting from irradiation or chemotherapy, and AIDS. SCF is also deficiency, sequence is a human SCF protein sequence (partial or full length).
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Sequence 245 AA;

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                                                                                                                                                                     MDVL.PSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
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100.0%; Score 1262; DB 8; Length 245; 100.0%; Pred. No. 3e-121; ive 0; Mismatches 0; Indels 0
                  Best Local Similarity 100.
Matches 245; Conservative
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ADS88051 standard; protein; 245 AA (first entry) 18-NOV-2004 ADS88051; RESULT 13

Tumour treatment-related human protein sequence SeqID87.

tumour inhibition, tumour treatment; metastasis; infectious lesion; antigen presenting cell; immunostimulatory cytokine; cytostatic; vulnerary; immunomodulator; melanoma; hepstoma; adenocarctinoma; colorectal cancer; bala cell cancer; oral cancer; nasopharyngeal cancer; bladder cancer; head cancer; neck cancer; neral cell cancer; palneratic cancer; pulmonary cancer; cervical cancer; ovarian cancer; oesophageal cancer; pulmonary cancer; cervical cancer; testicular cancer; breast cancer; human.

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ADU50663 standard; protein; 245

13-JAN-2005 (first entry)

ADU50663;

Homo sapiens

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This invention relates to a novel method of inhibiting or treating a tumour, metastasis or infectious lesion in a subject which comprises administrating into or near a site of a tumour or infectious lesion in a cubject an antigen presenting cell and an immunostimulatory cytokine or a nucleic acid encoding the cytokine. The invention may be useful for the production of compounds with a cytostatic or vulnerary activity acting as cumunomodulators. The method is useful in inhibiting or treating a cumunur, metastasis or infectious lesion in a subject, where the size of the tumour, metastasis (where number is also decreased) or infectious consistence in its selected from metanoma, hepatoma, adenocarcinoma, colorectal cancer, basal cell cancer, read and neck cancer, renal cell cancer, pancreatic cancer, pulmonary cancer, nearly cancer, pancreatic cancer, pulmonary cancer, cervical cancer, ovarian cancer and breast cancer, gastric cancer, prostrate.
                                                                                                                                                                                                                                                                                                 Inhibiting or treating a tumor, metastasis or infectious lesion comprises administering into or near site of a tumor or infectious lesion an antigen presenting cell and an immunostimulatory cytokine or a nucleic acid encoding the cytokine.
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                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 87; 169pp; English
                                                                            15-OCT-2003; 2003WO-US032827
                                                                                                                 15-OCT-2002; 2002US-0418865P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100. Matches 245; Conservative
                                                                                                                                                        (UYPI-) UNIV PITTSBURGH
                                                                                                                                                                                                  Lotze MT, Tahara H;
                                                                                                                                                                                                                                       WPI; 2004-365083/34.
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The invention relates to a stem cell factor (SCF) such as non-naturally-
cocurring SCF having an amino acid sequence sufficiently duplicative of
that of naturally occurring SCF to allow possession of a haematopoietic
biological activity of naturally occurring stem cell factor, or naturally
cocurring SCF. Also included are an isolated DNA sequence for use in
securing SCF. Also included are an isolated DNA sequence for use in
securing SCF. Also included are an isolated DNA sequence for use in
securing SCF. Also included are an isolated DNA sequence cell of non-
aturally occurring SCF, a prokaryotic or eukaryotic host cell
cransformed or transfected with the DNA, a polypeptide product of the
captression of the DNA in a prokaryotic or eukaryotic host
captression of non-naturally occurring SCF, a DNA sequence coding for a
polypeptide fragment or polypeptide analogue of naturally-occurring stem
cell factor, a biologically functional plasmid or viral DNA vector
including the DNA sequence above, a prokaryotic or eukaryotic host cell
stably transformed or transfected with the DNA, a polypeptide having part
or all of amino acid sequence encoded by composite nucleic acid sequence
cof human SCF cDNA sequence obtained from HT1080
cfibrosarcoma cell line, or human SCF cDNA sequence obtained from 537 bladder
carcinoma cell line (and having one or more of in vitro biological
cactivity of naturally-occurring stem cell factor, and an antibody
specifically binding SCF. SCF. is useful for traating leukopaenia,
chrombocytopaenia, anaemia, and enhancing engraffment of bone marrow
during transplantation in a mammal. SCF is useful enhancing bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel stem cell factor (SCF) such as non-naturally-occurring SCF or naturally occurring SCF, useful for treating leukopenia, thrombocytopenia, anemia, and enhancing engraftment of bone marrow during
                                                   Human; stem cell factor; SCF; haematopoietic;
HT1080 fibrosarcoma cell line; 5637 bladder carcinoma cell line;
Heukopaenia; Hromboortopaenia; anaemia; bone marrow during transplant;
bone marrow aplasia; myelosupression; immune deficiency; neoplasm;
nerve damage; infertility; intestinal damage;
                                                                                                                                                                myeloproliferative disorder: early haematopoietic progenitor cell; myeloproliferative disorders; aplastic anaemia; myelofibrosis; mayelosclerosis; metastatic carcinoma; multiple myeloma; Hodgkin's disease; lymphom; gaucher's disease; Niemann-Pick disease; Diamond-Blackfan anaemia; DBA; Fanconi's anaemia; gene therapy;
                 Human SCF cDNA from 5637 bladder carcinoma cell line, protein.
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90US-00573616.
90US-00589701.
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92US-00982255.
93US-00172329.
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07-AUG-2000; 2000US-00635249.
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SUGGS S V.
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(SUGG/) SUGGS S V.
(MART/) MARTIN F H.
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                                                                                                                                                                                                                                                                                  acute blood loss.
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cc recovery in treatment of radiation, chemical, or chemotherapeutic induced bone marrow aplasia or myelosuppression which involves treating patients with therapeutically effective doses of SCF. SCF is useful for treating acquired immune deficiency, neoplasia, nerve damage, infertility, intestinal damage, and a myeloproliferative disorder. SCF is useful for transfecting early haematopoietic progenitor cells with a gene which continving early haematopoietic progenitor cells with SCF, and transfecting a gene to a mammal which involves culturing early continued cells with a gene. SCF is useful for transfecting a gene to a mammal which involves culturing early continued cells with a gene. SCF is useful for treating various haematopoietic disorders, aplastic anaemia. CC myelofibrosis, myelomiatering the cultured cell to the mammal. SCF is useful for treating various haematopoietic disorders, aplastic anaemia, myelomiatering the cultured cell to the mammal. SCF is myelofibrosis, myeloma, Hodgkin's disease, lymphoma, Gaucher's anaemia. SCF is useful for enhancing the efficiency of gene therapy, for enhancing haematopoietic recovery after acute blood loss. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 GDSSLHWAAMALPALFSLIIGFAFGALYWKKRQPSLTRAVENIQINEEDNEISMLQEKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antianemic; Antiemetic; Cytostatic; Anti-HIV; Cardiovascular-Gen.; CNS-Gen.; Antiparasitic; Antibacterial; Immunosuppressive; Antiinflammatory; Fungicide; Antifertility; AIDS; aplastic anemia; paroxysmal nocturnal hemoglobinuria, osteopetrosis; acute leukemia; multiple myeloma; hodgkins disease; lymphoma; gauchers disease; multiple myelost, starcoidosis; plasmodium infection; vitamin deficiency; hypopigmentation; vitiligo; infertility; chronic myelocytic leukemia; cell proliferation; stem Cell Factor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1262; DB 8; Length 245;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                             sequence is a human SCF protein sequence.

    .25
    /label= Signal_peptide

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/label= Mature protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADW93108 standard; protein; 245 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 245; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 245 AA;
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The present invention relates to a method (M1) for stimulating proliferation of melanocyte cells in a human. (M1) involves administering proliferation of melanocyte cells in a human. (M1) involves administering to proliferation of melanocyte cells, and optionally a carrier, to that stimulates growth of melanocyte cells, and optionally a carrier, to the thuman. The SCP is covalently conjugated to a water soluble polymer e.g. polyethylene glycol. Also, the SCP is co-administered with one or more other cytokines. SCP is also able to stimulate the growth of primitive progenitors such as early hematopoietic progenitor cells that are capable of maturing to erythroid, megakaryocyte, granulocyte, creating promerries and macrophage cells, and non-hematopoietic stem cells such as collerating bone marrow regeneration, and in augmenting T cell accelerating bone marrow regeneration, and in augmenting T cell production. (M1) is useful for treating seem cells dusc to toxic, cradiant or immunological injury. (M1) is useful in treating AIDS, aplastic anemia, paroxysmal nocturnal hemoglobinuria, myelofibrosis, congestive splenomegaly, Kalaazar, sarcoidosis, primary of aplanic pancytopenia, disseminated fungus disease, fulminating septicemia, malaria, vitamin B12 and folic acid deficiency disease, pyridoxine deficiency disease, and hypopigmentation disorders such as competicemia, malaria, vitamin B12 and folic acid deficiency disease, intestinal damage resulting from irradiation or chemotherapy, and stem cell myeloproliferative disorders such as chronic myelogenic progenitors in syngeneic, allogeneic or autologous cell myelopotetic progenitors in syngeneic, allogeneic or autologous cerly hematopoletic progenitors in syngeneic, allogeneic or autologous therapy. The present sequence was used to illustrate the inventencent continued and acute leukemia, therapy. The present sequence was used to illustrate the inventencent continued and acute leukemia and acute leukemia malania and acute leukemia, and seem continued and acute leukemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stimulating proliferation of melanocyte cells in human, involves administering stem cell factor polypeptide or its biologically active fragments stimulating growth of melanocyte cells, and optionally carrier,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coding sequence for this protein was obtained from the 5637 bladder carcinoma cell line.
                                                                                                                                                                                                                                                                                                                                                                                Suggs SV, Martin FH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; SEQ ID NO 63; 212pp; English
                                                                                                                          89US-00422383.
90US-00537198.
90US-00573616.
90US-00589701.
91US-00684535.
92US-00982255.
                                                                                   2000US-00604325
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                                                                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC.
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                                                                                   26-JUN-2000;
US6852313-B1
                                                                                                                                                                                                                                                                                        24-MAY-1995;
                                       08-FEB-2005
                                                                                                                                                                                                                                                                   21-DEC-1993;
                                                                                                                               16-OCT-1989
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24-AUG-1990
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Query Match 100.0%; Score 1262; DB 9 Best Local Similarity 100.0%; Pred. No. 3e-121; Matches 245; Conservative 0; Mismatches 0

DB 9; Length 245; Indels 9

MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120

61

ઠ 윱 8

1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG

240 240 61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120 GDSSLHWAAMALPALFSLIIGFAFGALYWKKRQPSLTRAVENIQINBEDNEISMLQEKER GDSSLHWAAMALPALFSLIIGFAFGALYWKKRQPSLTRAVENIQINEEDNEISMLQEKER KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKGKAKNPP EFQEV 245 EFORV 245 121 181 181 241 241 121 셤 à 셤 Š 셤 ò 셤 This Page Blank (Uspto)

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US-10-620-642-63 1262 1 MKKTQTWILTCIYLQLLLFN......NBEDNEISMLQBKEREFQEV 245

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		mast cell growth f	m	mast cell growth f		Н	mast cell growth f		-	_	_	_			_	probable advanced	transcription init	hypothetical prote	conserved hypothet		•	hypothetical prote		secr		hypothetical prote	lactose transport	sodium channel SCA	formate dehydrogen
SUMMARIES	Q.	B61190	A35974	146575	A37934	847571	146929	865801	558313	B35974	S70367	JN0637	S70366	S29052	B35971	A35971	T09062	S37845	F82909	P90595	T37964	G86773	T23425	E90553	AD1507	ндвурн	AC2939	D98343	0	F64300
	DB	7	~	~	N	~	~	~	~	~	7	N	0	N	N	7	~	7	N	~	7	7	~	0	~	-	7	~	N	N
	Length	245	273	274	245	274	274	273	202	201	253	287	287	124	51	49	402	482	1447	647	3227	512	534	420	821	1174	295	309	1993	378
	Query Match	100.0	97.5	82.2	81.0	80.7	80.4	78.5	59.4	57.1	47.9	46.3	46.2	38.9	13.9	13.7	7.7	7.7	7.7	7.4	7.4	7.3	7.3	7.3	7.3	7.3	•	7.3	7.3	7.2
	Score	1262	1231	1037.5	1022	1018.5	1014.5		749.5	721	605	584	583	491.5	175.5	172.5	97.5	97	97	93.5	93.5	92.5	92.5	92	92	92	91.5	91.5	91.5	91
	Result No.	1	7	3	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25			28	29

ATP-dependent Clp	hypothetical prote	hypothetical prote	hypothetical prote	conserved hypothet	hypothetical prote	genome polyprotein	phosphoenolpyruvat	hypothetical prote	replication initia	hypothetical prote	hypothetical prote	phosphoenolpyruvat	hypothetical prote	hypothetical prote	hypothetical prote
A69136	T22309	S70770	C86613	B72012	T26656	RRVUBY	H84855	F71856	S74840	T19850	S51404	S26235	T27886	T19295	T22794
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616	774	1675	411	411	1384	2238	941	1154	447	246	570	996	1293	1813	099
7.2	7.2	7.2	7.1	7.1	7.1	7.1	7.0	7.0	7.0	6.9	6.9	6.9	6.9	6.9	6.9
90.5	90.5	90.5	90	90	89	89	88.5	88.5	88	87.5	87.5	87.5	87.5	87.5	87
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT	1 1
mast cell	mast call growth factor, short form precursor - human N/Alternate names: kit ligand, short form; stem cell factor, short form
C;Spec C;Date	C.Species: Homo aapiens (man) Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004 C.accesion: R61190
R; Ande	Characters. D. 1. Milliams, D.E.; Tushinski, R.; Gimpel, S.; Eisenman, J.; Cannizzaro, J.
A;Refe	ell Growth Diler. 2, 3/3-3/9, 1991. A.Title: Alternate spilcing of mRNAs encoding human mast cell growth factor and localiza A,Reference number: A61190, MUID:92172791, PMID:1724381
A; Acce	A;Accession: B61190 A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A; Mole	
A; Cros	A.Cross-references: UNIPROT:P21583; UNIPARC:UPI0000028351 C:Comment: Alternative splicing produces this short form in which a predicted cleavage
C, Genetics	
A; Gene A; Cros	Ajdene: GDB:nor AjCross-references: GDB:128026; OMIM:184745
A; Map	A;Map position: 12q22-12q22 C.Superfamily. monea mast cell growth factor
C, Key	C.Keywords.i
F; 187	Fil.23/DOMMAIN: bignar Sequence #sectus predicted <515. 18787-20/DOMMAIN: transmembrane #status predicted <tmn> Fig. 97 118 145/Binding site: carbohdrate (Bass) (covalent) #status predicted</tmn>
Oue	Ouery Match 100.0%; Score 1262; DB 2; Length 245;
Best	Similarity 100.0%; Pred. No. 4.8e-94; 5; Conservative 0; Mismatches 0; Indels
ò	1 MKKTQTWILTCIYLQLLLENPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKKVPG 60
qa	1 MKKTQTWILFCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKKVPG 60
ò	61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
ą	61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
ò	121 KDLKKSFKSPEPRLFTPEEPPRIFURSIDAFKDFVVASETSDCVVSSTLSPEKGKAKNPP 180
q	121 KDLKKSFKSPEPRLFTFEEFFRIFINKSIDAFKDFVVASETSDCVVSSTLSPEKGKAKOPP 180
È	181 GDSSLHWAAMALPALFSLIIGFAFGALYWKKRQPSLTRAVENIQINEBDNEISMLQEKER 240
q	181 GDSSLHWAAMALPALFSLIGFAFGALYWKKRQPSLTRAVENIQINBEDNEISMLQEKER 240
ò	241 BFQEV 245
q	241 BFQEV 245

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A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                         Best Local Similarity 75.29
Matches 206; Conservative
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Matches 198; Conservative
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             MESUNI 12
A15574
Masternate names: kit ligand; stem cell factor
C;Species: Home sapiens (man)
N;Alternate names: kit ligand; stem cell factor
C;Species: Home sapiens (man)
C;Species: Home sapiens (man)
C;Species: Home sapiens (man)
C;Dacession: A35974, M6I190
R;Matth, F. H; Sugge, S. V.; Langley, K. E.; Lu, H.S.; Ting, J.; Okino, K. H.; Morris, C. F
R;Matth, P. H; Sugge, S. V.; Langley, K. E.; Lu, H.S.; Ting, J.; Okino, K. H.; Morris, C. F
S, J. C.; Patel, A.C.; Fisher, E.F.; Erjavec, H.O.; Herrera, C.J.; Mypych, J.; Sachdev, R
A;Ttle: Primary structure and functional expression of rat and human stem cell factor I
A;Ttle: Primary structure and functional expression of rat and human stem cell factor I
A;Ttle: Primary structure and functional expression of rat and human stem cell factor I
A;Ttle: Primary structure and functional expression of rat and human stem cell factor I
A;Ttle: Primary structure and functional expression of rat and human stem cell factor I
A;Ttle: Attenace sumber: A15974; MUD:9100419; PMID:2208279
A;Cross-references: UNIPROT:P21831; MID:3172791; PMID:1724381
A;Accession: A61190
A;Accession: A61190
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A;Accession: A61190
A;Accession: A61190
A;Accession: A61190
A;Genetics: A61190
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A;Genetics: A61190
A;Genetics: A61190
A;Genetics: A61190
A;Cross-references: UNIPARC:UP100002D482
C;Genetics: A61190
A;Cross-references: UNIPARC:UP100002D482
C;Genetics: A61190
A;Cross-references: GDB:128026; OMIM:184745
A;Genetics: GDB:128026; OMIM:184745
A;Genetics: GDB:128026; OMIM:184745
A;Genetics: GDB:MA
A;Genetics: A61190
C;Genetics: A61190
A;Cross-references: GDB:128026; OMIM:184745
A;Genetics: GDB:128026; OMIM:184745
A;Genetics: GDB:128026; OMIM:184745
A;Genetics: GDB:MA
A;Ge
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146575

c-kit ligand - pig

C;Species: Sus scrofa domestica (domestic pig)

C;Species: Sus scrofa domestica (argumental pig)

C;Date: 2.7 Peb-1997 #sequence_revision 21-Peb-1997 #text_change 09-Jul-2004

C;Accession: 146575

R;Zhang, Z.; Anthony, R.V.

R;Zhang, Z.; Anthony, R.V.

R;Zhang, Z.; Anthony, R.V.

A;Title: Porcine stem cell factor/c-kit ligand: its molecular cloning and localization

A;Reference number: 146575; MUID:94146218; PMID:7508758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KDLKKSFKSPEPRLFTPEBFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKG----- 174
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Pred. No. 1.7e-91;
0; Mismatches 1;
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Best Local Similarity 89.4%;
Matches 244; Conservative
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A;Molecule type: mRNA
A;Residues: 1-274 «ZHA»
A;Cross-references: UNIPROT:Q29030; UNIPARC:UPI0000135640; GB:L07786; NID:g164420; PIDN:
C;Superfamily: mouse mast cell growth factor
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NyAlternate names: KL-2 protein
Cispecies: Mus musculus (house mouse)
Cjacies: Mus musculus (house mouse)
Cjacies: Mus musculus (house mouse)
Cjacies: 26-Jul-1991 #sequence_revision 26-Jul-1991 #text_change 09-Jul-2004
Cjaciesion: A37934; B43751
Cell 64, 1025-1035, 1991
A;Filanagan, J.G.; Chan, D.C.; Leder, P.
A;File: Transmembrane form of the kit ligand growth factor is determined by alternative A;Reference number: A37934; MUID:91160046; PMID:1705866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: A37934
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rossidues: 1-245 < CELA>
A;Cross-references: UNIPROT:P20826; UNIPARC:UPI000002B352; GB:M64262
A;Cross-references: UNIPROT:P20826; UNIPARC:UPI000002B352; GB:M64262
R;Huang, B.J; Nocka, K.H.; Buck, J.; Besmer, P.
A;Huang, B.J; Nocka, K.H.; Buck, J.; Besmer, P.
A;Hitle: Differential expression and processing of two cell associated forms of the kit-A;Reference number: A43751; MUID:92330001; PMID:1378327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 ENVKKSSKSPEPRLFTPEKFFGIFNRSIDAFKDLEMVAPKTSECVISSTLTPEKDSRVSV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211
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                                                                                                                                                                                                                                                                                                                                                              1 MKKTQTWIITCIYLQLLLFNPLVRTQGICRNRVTDDVKDVKLVANLFKDXKITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDF-VVASETSDCVVSSTLSPEKG----
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A;Residues: 1-173,'R',175-186,'L',188-245 <HUA>
A;Cross-references: UNIPARC:UP10000179560; GB:S04534
A;Note: the authors translated the codon TTG for residue 187 as Trp
C;Superfamily: mouse mast cell growth factor
                                                                                                                                                                     82.2%; Score 1037.5; DB 2; Length 274; 75.2%; Pred. No. 5.9e-76; ive 22; Mismatches 17; Indels 29;
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mast cell growth factor - mouse
N.Alternate names: hematopoietic growth factor KL; ligand steel factor; stem cell facto.
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: S63801; A43751; A35976; A35975; A35975; A35975; A35973; I48768
R;Bedell, M.A.; Copeland, N.G.; Jenkins, N.A.
A;Genetics 142, 927-934, 1996
A;Ritle: Multiple pathways for Steel regulation suggested by genomic and sequence analy.
A;Reference number: S65801; MUID:97002551; PMID:8849898
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A;Stetus: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: UNIPROT: P20826; UNIPARC: UPI0000028C9B; EMBL: U44725; NID: g1172215; P:
R;Huang, E.J.; Nocka, K.H.; Buck, J.; Besmer, P.
Mol. Biol. Cell 3, 349-362, 1992
A;Title: Differential expression and processing of two cell associated forms of the kit
A;Reference number: A43751; MUID: 92330001; PMID: 11378327
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A; Residues: 1-214, 'L', 216-273 <HUA>
A; Residues: 1-214, 'L', 216-273 <HUA>
A; Cross-references: UNIPARC:UP100001400C1; GB:S40364; NID:g251668; PIDN:AAB22554.2; PID
A; Note: the authors translated the codon TTG for residue 215 as Trp
R; Huang, E.; Nocka, K.; Beier, D.R.; Chu, T.Y.; Buck, J.; Lahm, H.W.; Wellner, D.; Leder
Cell 63, 225-233, 1990
A; Title: The hematopoietic growth factor KL is encoded by the Sl locus and is the ligan
A; Reference number: A35976; MUD:91004221; PMID:1698557
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-206,'S','208-270 eHU2>
A;Residues: 1-206,'S','208-270 eHU2>
A;Cross-references: UNIPARC:UP1000017955D; GB:M38511
B;Anderson, D.M.; Lyman, S.D.; Baird, A.; Wignall, J.M.; Bisenman, J.; Rauch, C.; March, Cell 63, 235-243, 1990
A;Title: Molecular cloning of mast cell growth factor, a hematopoietin that is active in A;Reference number: A35977; MUID:91004223; PMID:1698558
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: nTNA
A;Molecule type: mSNA
A;Cross-references: UNIPRRC:UPI0000028C9B; GB:MS7647; GB:M38436; NID:g199151; PIDN:AAA39
R;Cross-references: UNIPRRC:UPI000028C9B; GB:MS7647; GB:M38436; NID:g199151; PIDN:AAACG98101: A35972
A;Reference number: A35972; MUID:g1004216; PMID:1698554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 TKPFMLPPVAASSLRNDSSSSNRKASNSIGDSNLQWAAMALPAFFSLVIGFAFGALYWKK 240
                                                                                                                                                            MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
    9
                                          1 MKKTQTWIITCIYLQLLLFNPLVKTKGICGKRVTDDVKDVTKLVANLPKDYKIALKYVPG
1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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A;Molecule type: mRNA
A;Residues: 26-53 <COP>
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stem cell factor, longer isoform - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 27-40a-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C;Date: 27-40a-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C;Dates: 27-571
R;Zhou, J.H.; Hikono, H.; Ohtaki, M.; Kubota, T.; Sakurai, M.
Biochim. Biophys. Acta 1223, 148-150, 1994
A;Title: Cloning and characterization of cDNAs encoding two normal isoforms of bovine st
A;Teterence number: S47571; MUID:94339176; PMID:7520283
A;Reference number: S47571
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-274 <ZHO>
A;Residues: 1-274 <ZHO>
A;Cross-references: UNIPROT:Q28132; UNIPARC:UPIO000135639; EMBL:D28934; NID:9538520; PICC;Superfamily: mouse mast cell growth factor
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Cipate: O-45ep-1997 #sequence_revision 06-3ep-1997
Rishull, R.M.; Sugga, S.V.; Langley, K.E.; Okino, K.H.; Jacobsen, F.W.; Martin, F.H.
Exp. Hematol. 20, 118-1124, 1992
A;Title: Canine stem cell factor (c-kit ligand) supports the survival of hematopoietic p. A;Reference number: 146929
A;Accession: 146929
A;Accession: 146929
A;Accession: I46929
A;Accession: I46
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                         181 TKPFMLPPVAASSLRNDSSSSNRKASNSIEDSSLQWAAVALPAFFSLVIGFAFGAFYWKK 240
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                                                                                                                                                                                         241 EFQEV 245
                                                                                                                                                                                                                                                                 241 BFQEV 245
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Gaps

; 202;

Length Indels

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A;Residues: 1-202 <MCI>
A;Cross-references: UNIPROT:P79368; UNIPARC:UPI000016C4E5; EMBL:Z50743; NID:G940807; PID
C;Superfamily: mouse mast cell growth factor
                                                                                                                                                                                                                                                                                                                                          MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                      61 MDVLPSHCWISEMVEQLSVSLTDLLDKFSNISEGLSNYSIIDKLVKIVDDLVECMEEHSF 120
                                                                                                                                                                                                                                                            1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 59.4%; Score 749.5; DB 2; Best Local Similarity 83.9%; Pred. No. 5.5e-53; Matches 146; Conservative 15; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       stem cell factor protein precursor - rat (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: A39805
A;Status: preliminary
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A;Cross-references: UNIDARC:UP100001955B; GB:M59912
R;Zesbo, K.M.; Williams, D.A.; Geiseler, E.N.; Broudy, V.C.; Martin, F.H.; Atkins, H.L.; Cattanach, B.M.; Galidi, S.J.; Sugges, S.V.
Cattanach, B.M.; Galidi, S.J.; Sugges, S.V.
Cattanach, B.M.; Galidi, S.J.; Sugges, S.V.
A;Title: Stem cell factor is encoded at the Si locus of the mouse and is the ligand for A;Reference number: A35975; WUID:91004220; PMID:1698556
A;Accession: A35975
A;Accession: A35975
A;Residues: 1-201 - 2285-
A;Residues: 1-201 - 2285-
A;Residues: 1-201 - 2285-
A;Cross-references: UNIPARC:UP1000016D02D; GB:M59915; NID:g200935; PIDN:AAA40095.1; PID:
A; Langley, K.B.; Wyrych, J.; McNiece, I.K.; Lu, H.S.; Smith, K.A.; Karkare, S.B.; Sachdev, A.; Langley, K.B.; Myrych, J.; McNiece, I.K.; Lu, H.S.; Smith, K.A.; Karkare, S.B.; Sachdev, A.; Langley, K.B.; Protein:
A;Residues: 127-29; A;Assorial and Diological characterization of hematopoietic A;Researce number: A35973
A;Reternce number: A35973; MUID:91004218; PMID:2208278
A;Reternce number: Drotein
A;Residues: 27-29; R., 31-39 - 2522-
A;Reternce number: Drotein
A;Residues: 27-29; R., 31-39 - 2522-
B;Reternce number: A4071; MUID:9301294; MID:1383087
A;Reternce number: A4071; MUID:9301294; PMID:1383087
A;Reternce number: A4071; MUID:9301294; PMID:1383087
A;Reternce number: A4071; MUID:9301294; PMID:1383087
A;Residues: 1-206, S', 208-773 - RES>
A;Cross-references: UNIPARC:UPI000016CA07; EMBL:X68989; NID:9395283; PIDN:CAA48778.1; PMID:Sybertamily: mouse mast cell growth factor
C;Genetics:
C;Keywords: extracellular protein; 91ycoprotein; transmembrane protein
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C.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C.Date: 14-Jan.1996 #sequence_revision 01-Mar.1996 #text_change 09-Jul-2004
C.Accession: S58313
R.McInnes, C.J.; Logan, M.; Falconer, V.M.; Rawlins, P.; Huntly, J.; Haig, D. submitted to the EMBL Data Library, August 1995
A.Description: Molecular cloning and biological activity of ovine stem cell factor. A.Reference number: S58313
A.Accession: S58313
A.Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KDLKKSFKSPEPRLFTPEEFFRIFURSIDAFKDFVVASETSDCVVSSTLSPEKG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QSSLTRAVENIQINEEDNEISMLQQKEREFQEV 273
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C;Species: Rattus norregicus (Norway rat)
C;Date: 14-Dec-1990 #text_change 09-Jul-2004
C;Date: 14-Dec-1990 #text_change 0.7: Wypych, J.; Morris, C.F.
R;Martin, F.H.; Suggs, S.V.; Langley, K.E.; Lu, H.S.; Ting, J.; Okino, K.H.; Morris, C.F.
Call 63, 203-211, 1990
A;Title: Primary structure and functional expression of rat and human stem cell factor D
A;Reference number: A35974; MUID:91004219; PMID:2208279
A;Reference number: A35974
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: Text of the man of the molecule of the molecule type: Text of the molecule
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C;Species: Coturnix coturnix (quail)
C;Date: 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
C;Accession: 570367,
R;Petitte, J.N.; Kulik, M.J.
Biochim. Biophys. Acta 1307, 149-151, 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: /E',27-190 cLUA>
A;Cross-references: UNIPARC:UP1000014F57C
C;Superfamily: mouse mast cell growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 79.8% Matches 138; Conservative
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A, Molecule type: mRNA

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C; Superfamily: mouse mast cell growth factor
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Street cell factor precursor - chicken
C; Species: Gallus gallus (chicken)
C; Species: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C; Jaccession: JN0637
R; Zhou, J.H.; Ohtaki, M.; Sakurai, M.
Gene 127, 269-270, 1993
A; Title: Sequence of a cDNA encoding chicken stem cell factor.
A; Reference number: JN0637; MUID: 93273244; PMID: 7684722
A; Aritle: Sequence of a cDNA encoding chicken stem cell factor.
A; Residues: 1-287 cano.
A; Residues: 1-287 cano.
A; Residues: 1-287 cano.
A; Residues: 1-287 cano.
C; Superfamily: mouse mast cell growth factor
C; Keywords: growth factor; transmembrane prodicted cano.
F; 1-25/Domain: signal sequence #status predicted cano.
F; 226-281/Product: stem cell factor #status predicted cano.
F; 226-284/Domain: transmembrane #status predicted cano.
        fac
A; Title: Cloning and characterization of cDNAs encoding two forms of avian stem cell fa A; Reference number: $70366; MUID:96283808; PMID:8679698
A; Accession: $70367
A; Accession: $70367
A; Accession: $70367
A; Residues: 1-253 <-PET>
A; Residues: 1-253 <-PET>
A; Residues: 1-253 <-PET>
A; Cross-references: UNIPARC:UPI000002B34F; EMBL:U43079; NID:g1150877; PIDN:AACS9934.1; C; Superfamily: mouse mast cell growth factor
C; Keywords: growth factor; transmembrane protein
F; 1-25/Domain: signal sequence #status predicted <-SIG>
F; 26-253/Product: stem cell factor short form #status predicted <-MAT>
F; 192-216/Domain: transmembrane #status predicted <-TMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKRQP-SLTRAVENIQIN--EEDNEI 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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                                                                                                                                                                                                                                               Length 253;
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                                                                                                                                                                                                                                                                                       71; Indels
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                                                                                                                                                                                                                                             Query Match 47.9%; Score 605; DB 2; Best Local Similarity 49.8%; Pred. No. 2.9e-41; Matches 126; Conservative 48; Mismatches 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.3%; Score 584; DB 2; 44.6%; Pred. No. 1.7e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMLQEKEREFQEV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMLQQKEKEHLQV 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S:
Matches 128
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DKNKDFIKENGHUIBBURE...--GDSSIHWAMALPALFSLIIG 201
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C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S29052
R;Lu, S; Clogston, C.L.; Wypych, J.; Parker, V.P.; Lee, T.D.; Swiderek, K.; Baltera J.; Langley, K.E.
Arch. Biochem. Biophys. 298, 150-158, 1992
Arch. Biochem. Biophys. 298, 150-158, 1992
A;Title: Post-translational processing of membrane-associated recombinant human stem cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 1-13;14-30;31-46;47-59;60-86;87-95;96-107;108-124 <LUH>
A;Cross-references: UNIPROT:Q7M4N8; UNIPARC:UP10000179563; UNIPARC:UP10000179564; UNIPAF
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A;Reference number: S29052; MUID:92398336; PMID:1381905
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C;Species: Coturnix coturnix (quail)
C;Species: Coturnix coturnix (quail)
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C;Coturnix coturnix (quail)
C;Coturnix coturnix (quail)
R;Petiter, J.N.; Kulik, M.J.
B;Petiter, J.N.; Kulik, M.J.
B;Coturnix B;Ophys. Acta 1307, 149-151, 1996
B;Coturnix B;Ophys. Acta 1307, 149-151, 1996
B;Coturnix B;Ophys. Acta 1307, 149-151, 1996
B;Coturnix B;Ophys. Acta 13036
B;Coturnix B;Ophys. A;Coturnix B;Ophys. B;Ophys. Coturnix B;Ophys B;Ophys B;Coturnix B;Ophys B;Coturnix B;Ophys B;Coturnix B;Ophys B;Ophys B;Coturnix B;Ophys B;Ophys B;Ophys B;Coturnix B;Ophys 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MDVLPSHCWISEMVVQLSDSLTDLLDKF---SNISEGLSNYSIIDKLVNIVDDLVECVKE 117
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C.Keywords: growth factor; transmembrane protein
P;1-25/Domain: signal sequence #status predicted <SIG>
P;26-287/Product: stem cell factor long form #status predicted <MAT>
P;226-250/Domain: transmembrane #status predicted <TMM>
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44.3%; Pred. No. 2e-39;
ive 47; Mismatches 71; Indels 4
                                                                                                                                                                                                                                                                                                                                  241 FILGAIYWKKTHPKSRPESNETIQCHGCQEENEISMLQQKEKEHLQV
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Matches 127; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
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Job

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time : 21.2479 secs
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A35971
mag to the factor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 09-Jul-2004
C;Accession: A35971
C;Bates: 167-174, 1990
A;Title: Identification of a ligand for the c-kit proto-oncogene.
A;Reference number: A35971; MUID:91004215; PMID:1698553
A;Accession: A35971
A;Reference number: A35971, MUID:91004215; PMID:1698553
A;Accession: A35971
A;Accession: A35971
A;Reference: UNIPROT:P20826; UNIPARC:UP10000179561
C;Superfamily: mouse mast cell growth factor
C;Kcywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
B35971
mag to the factor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 09-Jul-2004
C;Accession: B35971
C;Accession: B35971
R;Williams, D.E.; Eisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park, I.R;Williams, D.E.; Eisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park, I.R;Hite: Identification of a ligand for the c-kit proto-oncogene.
A;Reference number: A35971; MUID:91004215; PMID:1698553
A;Accession: B35971
A;Restudues: 1-51.cWIL>
A;Residues: 1-51.cWIL>
A;Coss-references: UNIPROT:P20826; UNIPARC:UP10000179562
C;Superfamily: mouse mast cell growth factor
C;Keywords: transmembrane protein
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                                                                                                                                                                                                                                                            DKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSSKDLKKSFKSPEPRLFTPEEFFRIFN 145
                                                                                                                                                                              1 BGICRNRVTNNVK------30
                                                                                                                                             26 EGICRNRVINNVKDVTKLVANLPKDYMITLKYVPGMDVLPSHCWISEMVVQLSDSLTDLL 85
                                                                                                                                                                                                                                                                                             31 DKFSNISEGLSNYSII-----DDLVECVKENSSKOLKKSFKSPEPRLFTPEEFFRIFN 83
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Best Local Similarity 73.5%; Pred. No. 2e-07;
Matches 36; Conservative 4; Mismatches 6; Indels 3;
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                        Query Match 38.9%; Score 491.5; DB 2; Length 124; Best Local Similarity 72.3%; Pred. No. 1.5e-32; Matches 107; Conservative 0; Mismatches 0; Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
13.9%; Score 175.5; DB 2; Length 51;
Best Local Similarity 72.3%; Pred. No. 1.2e-07;
Matches 34; Conservative 5; Mismatches 7; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 ICGNPVTDNVXDITKLVANLPNDYMITLNYVAGMDVLPS-WWLDDMI 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 ICRNRVINNVKDVTKLVANLPKDYMITLKYVPGMDVLPSHCWISEMV 74
                                                                                                                                                                                                                                                                                                                                                                                                                   RSI----DFVVASETSDCVVSSTLSPEK 107
                                                                                                                                                                                                                                                                                                                                                                                  146 RSIDAFKDFVVASETSDCVVSSTLSPEK 173
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Search completed: February 22, 2006, 18:20:28

Thu

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245
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SCF_HUMAN
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086524 9F
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1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-1007 001-100
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rattus norv
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                                                                                                                        February 22, 2006, 18:05:51; Search time 126.212 Seconds (without alignments) 1369.555 Million cell updates/sec
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                                                                                                                                                                                                                                              1262
1 MKKTQTWILTCIYLQLLLFN......NBEDNBISMLQEKEREFQEV 245
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Q958d2
Q29030
Q29030
Q25813
Q95813
Q95818
Q95818
Q95818
P21581
P2086
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P2086
Q09108
Q091
5.1.7
Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                     2166443 segs, 705528306 residues
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Q68DZ2_HUMAN
SCF_RAT
SCP_MOUSE
SCP_SHEEP
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SCF HUMAN
SCF HORSE
SCF PELCA
SCF PIG
O54A14 RAT
SCF CAPHI
SCF BOVIN
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064384 9WURI
078ED8 MOUSE
SCF CHICK
SCF COTJA
061854 MOUSE
070408 HUMAN
08C9K1 MOUSE
09YGP2 AMBME
09YGP2 AMBME
09XGP2 AMBME
09XWO XEWIA
08C9K1 MOUSE
04SLA5 TETWG
085JH6 BRANE
04SLA5 TETWG
085JH6 BRANE
04SLA5 TETWG
GenCore version
Copyright (c) 1993 - 2006
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SCF_CANPA
SCP_MITOTION
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Maximum Match 100%
Listing first 45 summaries
                                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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length: 2000000000
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Match Length DB
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Maximum DB
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Q8mwp2 plasmodium Q8mwp1 plasmodium	Q8mwh2 plasmodium Q9mal4 arabidopsis	Q4z4q3 plasmodium O6ya77 plasmodium		Q8im40 plasmodium	Q5cla9 cryptospori			Q9p884 emericella	Q7yxx2 cryptospori
Q8MWP2_PLAFA Q8MWP1_PLAFA	Q8MWH2_PLAFA Q9MAL4_ARATH	Q4Z4Q3_PLABE O6YA77_PLARE	Q74191_LACJO	OSIM40 PLAF7	Q5CLA9_CRYHO	Q9LPD8_ARATH	O96VK6 EMENI	Q9P884 EMENI	Q7YXX2_CRYPV
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128	128 109	107.5	106	105.5	103.5	102.5	102.5	102.5	102.5
33	3.4 3.5	36 37	38	9 0	41	42	43	44	45

ALIGNMENTS

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181 GDSSLHWAAMALPALFSLIIGFAFGALYWKKRQPSLTRAVENIQINEEDNEISMLQEKER 240
181 GDSSLHWAAMALPAFFSLIIGFAFGALYWKKRQPSLTRAVENIQINEDDNEISMLQEKER 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecidae; Cercopithecinae; Papio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.4%; Score 1255; DB 2; Length 245; 99.2%; Pred. No. 1.1e-90; arive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
Kalina T., Storek J.;
Sabinated (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY226584; AAO72537.1; -; mRNA.
HSSP; P21583; LEXZ.
SMR; Q865Z4; 29-161.
GO; GO:0016020; C:nembrane; IEA.
GO; GO:000573; F:stem cell factor receptor binding; IEA.
GO; GO:0001573; P:eell adhesion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02404; SCF; 1.
SEQUENCE 245 AA; 27887 MW; 937B3CAF28D694FA CRC64;
                                                                 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
Stem cell factor.
Papio cynocephalus x Papio anubis.
             PRT;
QB65Z4 9PRIM PRELIMINARY;
Q865Z4;
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Matches 243; Conservative
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MEDLINE=22388257; PubMed=12477922; DOI=10.1073/pnas.24263899;
A Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A stapleton M., Soares M.B., Bonaldo M.P., Carainci P., Frange C.,
A Brownstein M.J., Usdin T.B., Toobhyuki S., Carainci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Halton B., Ketreman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smills D.E.,
Butterfield Y.S.N., McKapwinski M.I., Skalska U., Smills D.E.,
Butterfield Y.S.N., McKapwinski M.I., Marra M.A.,
Butterfield Y.S.N., McKapwinski M.I., Smills D.E.,
Butterfield Y.S.N., Krzywinski M.I., Marra M.A.,
Butterfield Y.S.N., McKapwinski M.I., Smills D.E.,
Butterfield Y.S.N., McKapwinski 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE (ISOFORM 2).
MEDLINE=99160429; PubMed=10049787; DOI=10.1006/bbrc.1999.0260;
Blair H.C., Julian B.A., Cao X., Jordan S.B., Dong S.S.;
"Parathyroid hormone-regulated production of stem cell factor in human osteoblasts and osteoblast-like cells.";
Bjochem. Biophys. Res. Commun. 255:778-784(1999).
                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                           WUCLECTIDE SEQUENCE (ISOFORM 1).
MEDLINE=91004219; PubMed=2208279; DOI=10.1016/0092-8674(90)90301-T;
Martin F.H., Suggs S.V., Langley K.E., Lu H.S., Ting J., Okino K.H.,
Morris C.F., McNiece I.K., Jacobsen F.W., Mendiaz B.A., Birkett N.C.,
Smith K.A., Johnson M.J., Parker V.P., Flores J.C., Patel A.C.,
Fisher E.F., Erjavec H.O., Herrera C.J., Wpych J., Sachdev R.K.,
Pope J.A., Leslie I., Wen D., Lin C.-H., Cupples R.L., Zsebo K.M.;
"Primary structure and functional expression of rat and human stem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92360843; PubMed=1379846;
Toyota M., Hinoda Y., Itoh F., Tsujisaki M., Imai K., Yachi A.;
"Expression of two types of kit ligand mRNAs in human tumor cells.";
Int. J. Hematol. 55:301-304(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE (ISOFORM 2).
PubMed=1724381;
Anderson D.M., Williams D.E., Tushinski R., Gimpel S., Eisenman J., Cannizzaro L.A., Aronson M., Croce C.M., Huebner K., Cosman D.;
"Alternate splicing of mRNAs encoding human mast cell growth factor and localization of the gene to chromosome 12q22-q24.";
Cell Growth Differ. 2:373-378(1991).
                  P21563; 016487; 0200K7.)
P21563; 016487; 0200K7.)
01-MAY-1991 (Rel. 18, Created)
01-MAY-2005 (Rel. 18, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (C.kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
Name=KITLG; Synonyme=MGF, SCF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Han C., Peng \vec{X}., Yuan J., Qiang B.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE OF 167-248 (ISOFORM 2).
   273 AA
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell factor DNAs.";
Cell 63:203-211(1990)
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Isold=P21533-2; Sequence=VSP 006022;
DEVELOPMENTAL STAGE: Acts in the early stages of hematopoiesis.
DEVELOPMENTAL STAGE: Acts in the early stages of hematopoiesis.
PTM: A soluble form is produced by proteolytic processing of isoform 1 in the extracellular domain.
SIMILARITY: Belongs to the SCF family.
DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
WWW="http://www.infobiogen.fr/services/chromcancer/Genes/MGFID142.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Cycoplasmic (Potential).
N-linked (GlCNAc. .) (Potential).
By similarity.
By similarity.
By similarity.
Fy similarity.
Fy similarity.
Fy similarity.
Fy similarity.
Fy similarity.
augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins.
SUBGNIT: Homodimer, non-covalently linked (Probable).
SUBGELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2). Also exists as a secreted soluble form (isoform 1 only) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTIGEVSP_006022.

55 L -> S (in Ref. 3 and 4; AAK92486).

128 K -> R (in Ref. 3 and 4; AAK92486).

134 L -> F (in Ref. 3 and 4; AAK92486).

30899 MW; 19FD362CB59C6607 CRC64;
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GO; GO:0005886; C:plasma membrane; NAS.

GO; GO:0008283; P:cell proliferation; TAS.

GO; GO:0008283; P:cell proliferation; TAS.

GO; GO:0001065; P:nemopolesis; NAS.

GO; GO:0007165; P:signal transduction; TAS.

InterPro; IPR01251; Cytokine 4 hlx.

InterPro; IPR00355; SCF:

PANTHER; PTRR1574; SCF:

PEam; PP02404; SCF: 1.
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                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=2;
Name=1; Synonyms=SCF248;
IsoId=P21583-1; Sequence=Displayed;
Name=2; Synonyms=SCF220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; MS9964; AAA85450.1; -; mRNA.
EMBL; AF119835; AAA022048.1; -; mRNA.
EMBL; AF400436; AAK02485.1; -; mRNA.
EMBL; AF400437; AAK02486.1; -; mRNA.
EMBL; BC069733; AA469783.1; -; mRNA.
EMBL; BC069783; AA469783.1; -; mRNA.
EMBL; BC069783; AA469783.1; -; mRNA.
EMBL; BC074725; AA47725.1; -; mRNA.
EMBL; BC190; AA46797.1; -; mRNA.
EMBL; BC190; AA46797.1; -; mRNA.
EMBL; AS5974; AA5974.
PIR; B61190; B61190.
PIR; B61190; B61190.
PIR; BC1190; B61190.
ENGREMD1; ENSG00000049130; Homo sapiens.
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ALTERNATIVE PRODUCTS:
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MIM; 184745; -.
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A Murray J.D., Bowling A.T.;
A primary Human-Horse comparative gene map.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).

-!- SUBGLIULAR LOCATION: Type I membrane protein. Also exists as a secreted soluble form (By similarity).

-!- TYM: A soluble form (By similarity).

-!- FTM: A soluble form is produced by proteolytic processing of the extracellular domain (By similarity).

-!- SIMILARITY: Belongs to the SCF family.
                                                                              MKKTQTWILTCIYLQLLLENPLVKTEGICRNRVTNNVKOVTKLVANLPKDYMITLKYVPG
                                                                                                                                        MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                                                                                                             -------KAKNPPGDSSLHWAMALPALFSLIIGFAFGALYWKKR
                                                                1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                        MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                                                                                                KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKG----
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                                        Gaps
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
Name=KITLG; Synonyms=MGF, SCF;
Equus caballus (Horses).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Skin; steed=Cortes M.L., Joerg H., Stranzinger G.; steeder S., Checa-Cortes M.L., at equine sequence homologous to stem cell factor (KIT-ligand)."; submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
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                                        28;
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Terry R.R., Mickelson J.R., Schmutz S., Cothran E.G., Bailey "Egrus caballus mast cell growth factor (MGF).";
Submitted (JUL-201) to the EMBL/enBank/DDBJ databases.
             Length 273;
                                        Indels
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          Score 1231; DB 1;
Pred. No. 9.4e-89;
0; Mismatches 1;
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        97.5%;
        Query Match
Best Local Similarity 89.4
Matches 244; Conservative
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Suropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Potential.

Kit ligand.

Extracellular (Potential).

Potential.

Cytoplasmic (Potential).

N-linked (GlCNAc. .) (Potential).

My similarity.

By similarity.

By similarity.

Missing (in Ref. 2).

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P79169;
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2003 (Rel. 47, Last annotation update)
110-MAY-2005 (Rel. 47, Last annotation (SCF) (Mast cell growth factor) (Mast actor) (Mast acto
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19; Mismatches 16; Indels
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96C1D4C9059132F2 CRC64;
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EMBL; AF053498; AAC97076.1; -; mRNA.

EMBL; AF367704; AAK63249.1; -; Genomic_DNA.

EMBL; AF307706; AAK63250.1; -; Genomic_DNA.

EMBL; AF307706; AAF36716.1; -; Genomic_DNA.

EMBL; AF130770; AAF36716.1; -; Genomic_DNA.

INTEXPRO; IPR012351; Cytokine_4_hlx.

INTEXPRO; IPR003452; SCF.

INTEXPRO; PTHR11574; SCF; 1.
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Pfam; PF02404; SCF; 1.
Cell adhesion; Glycoprotein; SIGMAL
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SCE_RELCA
SCE_RELCA
AC P7916
DT 28-FB
DT 28-FB
DT 10-MA
DB Kit 1
DB Kit 1
CAN Name:
OC Bukar
OC Bukar
OC Rukar
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EMBL, 107786; AAA53670.1; -; mRNA.
PIR; 146575; 146575.
SWR; Q29030; 29-161.
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                                                                                                                       STANDARD;
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NUCLEOTIDE SEQUENCE.
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Best Local Similarity
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                                                                      DNA Seq. 6:233-237(1996).

-I- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).
-I- SUBGELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2). Also exists as a secreted soluble form (isoform 1 only) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                    NUCLECTIDE SEQUENCE (ISOFORMS 1 AND 2).
MEDLINE=9706946; PubMed=8912926;
Dunham S.P., Onions D.E.;
"The cloning and sequencing of cDNAs encoding two isoforms of feline stem cell factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G (in
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N-linked (GloNAc. .) (Potential).
N-linked (GloNAc. .) (Potential).
N-linked (GloNAc. .) (Potential).
N-linked (GloNAc. .) (Potential).
By similarity.
By similarity.
DSRVSVTKPFMLPPVAASSIRNDSSSSNR -> G (in
                                                                                                                                                                                                                                                                                                                                                                 EMBL, D50833; BAA09445.1; -; mRNA.
SMR; P79169; 29-161.
InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR003452; SCF.
PANTHER, PTRA11574; SCF.
PATER PRO2404; SCF; 1.
Alternative splicing; Cell adhesion; Glycoprotein; Growth factor; Signal; Transmebrana.
Signal; Transmebrana.
SiGNAL.
                                                                                                                                                                                                                                               IsoId=P79169-2; Sequence=VSP 006021;
-!- PTM: A soluble form is produced by proteolytic processing of
  isoform 1 in the extracellular domain (By similarity).
-!- SIMILARITY: Belongs to the SCF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kit ligand.
Extracellular (Potential).
Potential.
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C5B78DB4791237BE CRC64;
                                                                                                                                                                                                  Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                            IsoId=P79169-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    isoform 2)
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                                                                                                                                                              181 TKPFMLPPVAASSLRNDSSSSNRKATNPIEDSSIQWAVMALPACFSLVIGFAFGAFYWKK 240
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Zhang Z., Anthony R.V.;

Zhang Z., Zhang
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Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-MXY-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
Name-KITLG; Synonyms-MGF;
Sus scrofa (Pig).
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Kit ligand.

Extracellular (Potential).

Extracellular (Potential).

Cytoplasmic (Potential).

N-linked (GloNAc. .) (Potential).

N-linked (GloNAc. .) (Potential).

N-linked (GloNAc. .) (Potential).

By similarity.

By similarity.
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No. 1.7e-73;
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InterPro; IPR003452; SCF.
PANTHER; PTHR11574; SCF; 1.
Pfam; PF02404; SCF; 1.
Cell adhesion; Glycoprotein; Growth formal and signal and sign
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                                                                    MDVLPSHCWISEMVEQLSVSLTDLLDKFSNISEGLSNYSIIDKLVKIVDDLVECMEEHSF 120
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                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Bukaryota; Metazoa; Metazoa; Chordata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
 Gaps
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MEDLINE-22831116; PubMed=12951073; DOI=10.1016/j.bbrc.2003.08.025;
Hirokawa Y.S., Watanabe M., Shiraishi T.;
Hirokawa Y.S., Watanabe M., Shiraishi T.;
The 3'UTR of stem cell factor suppresses protein expression from a cotransfected vector.";
Biochem. Seguence 245 Aa; 27681 MW; 9615130876AC9052 CRC64;
 29;
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81.1%; Score 1023; DB 2; Length 245;
Best Local Similarity 80.4%; Pred. No. 2e-72;
Matches 197; Conservative 18; Mismatches 30; Indels
 Indels
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Stem cell factor KL-2.
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22; Mismatches
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206; Conservative
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Q54A14;
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                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (Crit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
Name=KITLG; Synonyms=SCF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kit ligand.

Kit ligand.

Extracellular (Potential).

Potential.

Cytoplasmic (Potential).

N-linked (GloNAc. .) (Potential).

N-linked (GloNAc. .) (Potential).

N-linked (GloNAc. .) (Potential).

N-linked (GloNAc. .) (Potential).

By similarity.

By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Growth factor; Signal; Transmembrane
                                                                                                                              Capra hircus (Goat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi.
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.9%; Score 1021.5; DB 1; Length
74.5%; Pred. No. 3e-72;
ive 20; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BBFE669A509EF65D CRC64;
274 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB002152; BAB71753.1; -; mRNA. SNR; Q95M19; 29-161.
InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR003452; SCF.
PANTHER; PTHR11574; SCF; 1.
PÉam; PF02404; SCF; 1.
                                                                                                                                                                            Pecora; Bovidae; Caprinae; Capra.
NCBI_TaxID=9925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 N-
196 N-
114 By
164 By
31053 MW;
                                                                                                                                                                                                                                                   STRAIN=Shiba; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 74.5%
Matches 204; Conservative
STANDARD;
                                                                                                                                                                                                                   [1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           274 AA;
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CAPHI
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TRANSMEM
TOPO DOM
CARBOHYD
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DISULFID
SEQUENCE
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CARBOHYD
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                             181 TKPFMLPPVAASSLRNDSSSSNRKASNSIEDSSLQWAAVALPAFFSLVIGFAFGALYWKK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Table-Q28132-2; Sequence=VSP 006020;
PTM: A soluble form is produced by proteolytic processing of
isoform 1 in the extracellular domain (By similarity).
POLYMORPHISM: The roan locus is responsible for the coat
coloration of Belgian Blue and Shorthorn cattle. The solid-colored
and white animals are homozygotes, and the roan animals, with
intermingled colored and white hairs, are heterozygous. The roan
phenotype is due to the Asp-218 mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Belgian Blue;

MEDLINE=99315331; PubMed=10384045; DOI=10.1007/8003359901076;

MEDLINE=99315331; PubMed=10384045; DOI=10.1007/8003359901076;

MEDLINE=99315331; PubMed=10384045; DOI=10.1007/8003359901076;

MEDLINE=99315331; PubMed=10384045; DOI=10.1007/8003359901076;

The missense mutation in the bovine MGP gene is associated with the roan phenotype in Belgian Blue and Shorthorn cattle.";

Mamm. Genome 10:710-712(1999).

I. FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).

-!-SUBGELLUIAR LOCATION: Type I membrane protein (isoforms 1 and 2).

Also exists as a secreted soluble form (isoform 1 only) (By similarity).
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                                                                       ---KAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-94339176; PubMed=7520283; DOI=10.1016/0167-4889(94)90084-1; Zhou J., Hikono H., Ohtaki M., Kubota T., Sakurai M.; "Cloning and characterization of cDNAs encoding two normal isoforms bovine stem cell factor."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mediates also
                                                                                                                                                                                                                            SCF BOVIN STANDARD; PRT; 274 AA.
028132; O9TU74;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (C-kit ligand) (Stem cell factor) (NGF).
Name-KITLG; Synonyms-SCF;
Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kudo T.;
"Bovine counterpart of stem cell factor.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE OF 204-239, AND VARIANT ASP-218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=2;
                                                                                                                              ROPSLTRAVENIQINEEDNEISMLQEKEREFQEV 245
                                                                                                                                             241 KQPNLTRTVENRQINEEDNEISMLQEKEREFQEV 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=Q28132-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochim. Biophys. Acta 1223:148-150(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTERNATIVE PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Fetal brain;
                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Spleen;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                Kit ligand.

Extracellular (Potential).

Extracellular (Potential).

Cytoplasmic (Potential).

N-linked (GlcNAc. . .) (Potential).

N-linked (GlcNAc. . .) (Potential).

N-linked (GlcNAc. . .) (Potential).

By similarity.

By similarity.

By similarity.

By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 MDVLPSHCWISEMVEQLSVSLTDLLDKFSNISEGLSNYCIIDKLVKIVDDLVECMEEHSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 KOLKKSFKSPEPRLFTPEEFPRIFNRSIDAFKDF-VVASETSDCVVSSTLSPEKG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ENVKKSSKSPEPRQFTPEKFFGIFNKSIDAFKDLBIVASKMSECVISSTSSPEKDSRVSV
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01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
11 Again precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast
Cell growth factor) (MGF).
Name=KXILG; Synonyms=MGF;
Canis familiaris (DOG).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Leurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                     EMBL; D28934; BAA06061.1; -; mRNA.

EMBL; AB033716; BAA94808.1; -; mRNA.

FMRL; AR120154; AAD55355.1; -; Genomic_DNA.

FMRL; A8120154; AAD55355.1; -; Genomic_DNA.

SMR; Q28132; 29-161.

SMR; Q28132; 29-161.

InterPor; IPR012351; Cytokine_4_hlx.

InterPor; IPR013551; Cytokine_4_hlx.

PANTHER; PTHR1574; SCF; 1.

Pfam; PF0404; SCF; 1.

Pfam; PF0404; SCF; 1.

Polymorphism; Iransmembrane.

SIGNAL

SIGNAL
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A -> D (in roan allele).
D6C1DDB77B0CB12B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROPSLTRAVENIOINEEDNEISMLOEKEREFOEV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 80.7%; Score 1018.5; DB Best Local Similarity 74.1%; Pred. No. 5.2e-72; Matches 203; Conservative 20; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274 AA
SIMILARITY: Belongs to the SCF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isoform 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 218 P 274 AA; 31015 MW;
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SEQUENCE
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SCF_CANFA
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                                           181 TKPFWLPPVAASSLRNDSSSSNRKASNSIGDSNLQWAAMALPAFFSLVIGFAFGALYWKK 240
  121 ENVKKAPKSPELRLFTPEBFFRIFNRSIDAFKOLBTVASKSSECVVSSTLSPDKOSRVSV 180
                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Mustelidae;
                               ---KAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKK
                                                                                                                                                                                                                                                                                                                                                                                            Bennett R.D., Murphy B.D.;
Submitted (WOV-2000) to the EMBL/GenBank/DDBJ databases.

-!-FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).

-!-SUBCELIULAR LOCATION: Type I membrane protein. Also exists as a secreted soluble form (By similarity).
                                                                                                                                                                                           Q9SN18; Q9SNN5;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 47, Last annotation update)
Kit ligand precursor (C-Kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
Name=KITLG; Synonyms=SCF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AY013712; AAG37434.1; -; mRNA.
EMBL; AF323757; AAK73366.1; -; mRNA.
SMR; Q950118; 29-161.
InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR03452; SCF.
PANTHER; PTRR1574; SCF; 1.
Pfam; PF0464; SCF; 1.
Alternative splicing; Cell adhesion; Glycoprotein; Growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isold=Q9SN18-2; Sequence=VSP 006024;
-!- PTW: A soluble form is produced by proteolytic processing of isoform 1 in the extracellular domain (By similarity).
-!- SIMILARITY: Belongs to the SCF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Potential) . (Potential) . (Potential) .
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Extracellular (Potential).

Potential.

Cytoplasmic (Potential).

N-linked (GlcNAc. . .) (Potential).
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                                                                                    245
                                                                                                              274
                                                                                    ROPSLTRAVENIOINEEDNEISMLOEKEREFOEV
                                                                                                  241 KOPNLTRTVENIQINEEDNBISMLOEKEREFOEV
                                                                                                                                                                                  274 AA
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                                                                                                                                                                                                                                                                                               Mustela vison (American mink).
                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal; Transmembrane
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                        Mustelinae; Mustela.
                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9667;
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TRANSMEM
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MDVLPSHCWISVWVEQLSVSLTDLLDKFSNISEGLSNYSIIDKLVKIVDDLVECTEGYSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                    -!- DEVELOPMENTAL STAGE: Acts in the early stages of hematopoiesis.
-!- PTM: A soluble form is produced by proteolytic processing of the extracellular domain (By similarity).
-!- SIMILARITY: Belongs to the SCP family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29; Gaps
                                                                                                                                                                                          probably interleukins.
SUBUNIT: Homodimer, non-covalently linked (Probable).
SUBCELLULAR LOCATION: Type I membrane protein. Also exists as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Growth factor; Signal; Transmembrane
                                                                          (GlCNAc. .) (Potential)
(GlCNAc. .) (Potential).
(GlCNAc. .) (Potential).
(GlCNAc. .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 274;
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Extracellular (Potential).
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Cytoplasmic (Potential).
N-linked (GlCNAC. . ) (F
S similarity.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, S53329; AAB24619.1; -; mRNA.
EMBL, AY094361; AAM16280.1; -; mRNA.
PIR; 146929; 146929.
SWR, O66220; 29-161.
Ensembl; ENSCAF00000006091; Canis familiaris.
InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR03452; SCP.
PANTHER; PTHR11574; SCF; 1.
Pfam; PF02404; SCF; 1.
Cell adhesion; Glycoprotein; Growth factor; Signa SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93106145; PubMed=1281786;
                                                                                                                                                                  NUCLEOTIDE SEQUENCE OF 17-274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30870 MW;
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Best Local Similarity 74.8
Matches 205; Conservative
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215
238
274
                                        NUCLEOTIDE SEQUENCE.
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196
29
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68
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274 AA;
Canis.
NCBI_TaxID=9615;
                                                       TISSUE=T-cel]
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TRANSMEM
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CARBÖHYD
CARBOHYD
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factor DNAs.";
63:203-211(1990)
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                                                                                              164
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                                                                                                                                                                                                                                                                                                                                                                      181 TKPFMLPPVAASSLRNDSSSSNRKAANPLGDSNLQWAAMALPAFFSLVIGFAFGALYWKK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 VANLPKDYMITLKYVPGMDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDK 103
                                                                                                                                                                                                                                                                                                                                                                                                                              KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDF-VVASETSDCVVSSTLSPEKG---- 174
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
                                                                                                                                                                                                                                                                                          1 MKKTQTWIITCIYLQLLLFNPLVRTKGICRNRVTDDVKDVKLVANLPKDYKIALNYVPG
                                    isoform 2).
/FIId=vSp 006024.
S -> P (in Ref. 1; AAK73366).
S -> N (in Ref. 1; AAK73366).
S -> N (in Ref. 1; AAK73366).
EREFQEV -> RESFKRCNCGFYHTVLSYLGG (in Ref.
                                                                                                                                                                                                                                                                      1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                  MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
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                      (in
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                                                                                                                                                                                          80.4%; Score 1014.5; DB 1; Length 274; 73.7%; Pred. No. 1.1e-71;
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By similarity.
DSRVSVTKPFMLPPVAASSLRNDSSSSNR
                                                                                                                                                                                                              ; Pred. No. 1.1e-71;
20; Mismatches 23; Indels
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                                                                                                                                  1; AAK73366).
5AC1619014AE5E72 CRC64;
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Last annotation update)
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25-OCT-2004 (TrEMBLrel. 28, Last seq.
25-OCT-2004 (TrEMBLrel. 28, Last ann
Hypothetical protein DKFZp686F2250.
Name=DKFZp686F2250;
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0016020; C:membrane; IEA.
GO; GO:0005173; F:stem cell factor re
GO; GO:0007155; P:cell adhesion; IEA.
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                                                                                                                                                        MW.
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The German cDNA Consortium;
                                                                                                                                                        31035
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hes 202; Conservative
  164
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274
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171
268
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DISULFID
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                                                                          CONFLICT
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                                                                                                                                                        SEQUENCE
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195
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LVNIVDDLVECVKENSSKOLKKSPKSPEPRLFTPEEFPRIFNRSIDAFKDFVVASETSDC
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MEDLINE-91217037; PubMed-1708771;
Lu H.S., Clogaton C.L., Wypych J., Fausset P.R., Lauren S.,
Mendiaz E.A., Zsebo K.M., Langley K.E.;
"Amino acid sequence and post-translational modification of stem cell
factor isolated from buffalo rat liver cell-conditioned medium.";
J. Biol. Chem. 266:8102-8107(1991).
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MEDLINE-910.04219; Pubmed=2208279; DOI=10.1016/0092-8674 (90) 90301-T;
Martin F.H., Suggs S.V., Langley K.E., Lu H.S., Ting J., Okino K.H.,
Morris C.F., McNiece I.K., Jacobsen F.W., Mendiaz B.A., Birkett N.C.,
Smith K.A., Johnson M.J., Parker V.P., Flores J.C., Patel A.C.,
Fisher E.F., Erjavec H.O., Herrera C.J., Wypych J., Sachdev R.K.,
Pope J.A., Leslie I., Wen D., Lin C.-H., Cupples R.L., Zsebo K.M.;
Primary structure and functional expression of rat and human stem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFIDE
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-!- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins.
-!- SUBUNIT: Homodimer, non-covalently linked (Probable).
-!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2). Also exists as a secreted soluble form (isoform 1 only) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91004218; PubMed=2208278; DOI=10.1016/0092-8674(90)90300-4; Zsebo K.M., Wypych J., McNiece I.K., Lu H.S., Smith K.A., Karkare S.B., Sachdev R.K., Yuschenkoff V.N., Birkett N.C., Williams L.R., Satyagal V.N., Tung W., Bosselman R.A., Mendiaz B.A.,
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                                                                                                                                                                                                                                                                                                                                      245
                                                                                                                                                                                                                                                                                                                                      196 FSLIIGFAFGALYWKKRQPSLTRAVENIQINEEDNEISMLQEKEREFQEV
                                                                                                                                                                                                                                                                                                                                                                                 FSLIIGFAFGALYWKKRQPSLTRAVENIQINEEDNEISMLQEKEREFQEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Teramoto T., Nagashima M., Thorgeirsson S.S.; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P21581; Q9QwZ4; Q9Z2E7;
01-MAY-1991 (Rel. 18, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (C-kit ligand) (Stem cell factor)
cell growth factor) (MGF) (Hematopoietic growth factor
Name-Kitlg; Synonyms-Mgf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             273 AA
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factor)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 KPFMLPPVAASSLRNDSSSSNRKAAKSPEDPGLQWTAMALPALISLVIGFAFGALYWKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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                                          Alternative splicing, Cell adhesion, Direct protein sequencing; Glycoprotein; Growth factor; Pyrrolidone carboxylic acid; Signal; Transmembrane.
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Extracellular (Potential).

Potential.

Cytoplasmic (Potential).

Pyrrolidone carboxylic acid.

N-linked (GlCNAc. . .); partial.

O-linked (Probable).

O-linked (Probable).

O-linked (Probable).

N-linked (Probable).

N-linked (Probable).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isoform 2).
/Prid='VSP 006025.
S - P (in Ref. 1; AAD02828).
COF56527DC93FD27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31; Indels
similarity).
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                      Ensembl; ENSRNOG0000005386; Rattus norvegicus.
InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IRR03452; SCF.
PANTHER; PTHR11574; SCF; 1.
PERM; PF02404; SCF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.6%; Score 992; DB 1;
71.8%; Pred. No. 6.4e-70;
iive 18; Mismatches 31;
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                                                                                                                                                                                                                                                                                           EMBL; AF071204; AAD02827.1; -; mRNA.
EMBL; AF071205; AAD02828.1; -; mRNA.
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PIR; B35974; B35974.
SMR; P21581; 29-159.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91004223; PubMed=1698558; DOI=10.1016/0092-8674(90)90304-W; Anderson D.M., Lyman S.D., Baird A., Wignall J.M., Eisenman J., Rauch C., March C.J., Boswell H.S., Gimpel S.D., Cosman D., Williams D.E.;
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PRT; 273 AA.
202624; 062524; 06222; 0921N5;
01-FEB-1991 (Rel. 17, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-1005 (Rel. 47, Last annotation update)
Kit ligand breursox (C.kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF) (Hematopoietic growth factor KL) (Steel
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241 QSSLTRAVENIQINBEDNEISMLQQKEREFQEV 273
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"Differential expression and processing of t
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STRAIN-WCB6F1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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                            5 of the murine Mgf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
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[11] NUCLEOTIDE SEQUENCE OF 1-201.

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKKTOTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
MEDLINE=91004220; PubMed=1698556; DOI=10.1016/0092-8674(90)90302-U; Zsebo K.M., Williams D.A., Geissler E.N., Broudy V.C., Martin F.H., Jackins H.L., Heu R.-Y., Birkett N.C., Okino K.H., Murdock D.C., Jacobsen F.W., Langley K.E., Smith K.A., Takeishi T., Cattanach B.M., Galli S.J., Suggs S.V.; Rem cell factor is encoded at the Sl locus of the mouse and is the ligand for the c-kit tyrosine kinase receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins. Covalently linked (Probable) SUBCELULAR LOCATION: Type I membrane protein (isoforms I and 2). Also exists as a secreted soluble form (isoform I only) (By
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                                                                                                                                                                                                                                                                                                                                                                           PARTIAL PROTEIN SEQUENCE OF 26-78.

MEDLINE=91004215; PubMed=1698553; DOI=10.1016/0092-8674(90)90297-R; Williams D.E., Elsenman J., Baird A., Rauch C., van Ness K., March C.J., Park L.S., Martin U., Mochizuki D.Y., Boswell H.S., Burgess G.S., Cosman D., Lyman S.D.; "Identification of a ligand for the c-kit proto-oncogene."; Cell 63:167-174(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stages of hematopoiesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISOId=P20826-2; Sequence=VSP 006023;
-1- DEVELOPMENTAL STAGE: Acts in the early stages of hematopoies:
-1- FTM: A soluble form is produced by proteolytic processing of isoform 1 in the extracellular domain.
-1- SIMILARITY: Belongs to the SCF family.
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EMBL, U44724; -; NOT ANNOTATED CDS; Genomic_DNA.
EMBL, U44725; AAC52447.1; -; mRNA.
EMBL, X95381; CAA44667.1; -; mRNA.
EMBL, X99322; CAA64667.1; -; mRNA.
EMBL, X99322; CAA67698.1; -; mRNA.
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IsoId=P20826-1; Sequence=Displayed;
Name=2; Synonyms=KL-2;
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EMBL; M57647; AAA39538.1; -; mRNA.
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Matches 197; Conservative
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ALTERNATIVE PRODUCTS:
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181 KPFMLPPVAASSLRNDSSSSNRKAAKAPEDSGLQWTAMALPALISLVIGFAFGALYWKKK
                                                              ------KAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTM: A soluble form is produced by proteolytic processing of the extracellular domain (By similarity). SIMILARITY: Belongs to the SCF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).
SUBUNIT: Homodimer, non-covalently linked (Probable).
SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a secreted soluble form (By similarity).
                                                                                                                                                                                                                                                                                                   SCF_SHEEP
P97368; Q28591;
29-FEB-2003 (Rel. 41, Created)
29-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2003 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation)
10-MAY-2005 (Sheep)
10-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE OF 1-202.
MEDLINE-99263397; PubMed=10328863; DOI=10.1006/cyto.1998.0430;
MEDLINE-99263397; PubMed=10328863; DOI=10.1006/cyto.1998.0430;
MICTINES C.J., Deane D., Thomson J., Broad A., Haig D.M.,
"The cloning and expression of the cDNA for ovine stem cell factor (kit-ligand) and characterization of its in vitro haematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Growth factor; Signal; Transmembrane. Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Ovarian follicle;
MEDLINE=96413880; PubMed=8662240; DOI=10.1007/s003359900142;
Tisdall D.J., Quirke L.D., Galloway S.M.;
Torine stem cell factor gene is located within a syntenic group chromosome 3 conserved across mammalian species.";
Mamm. Genome 7:472-473(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kit ligand.
Extracellular (Potential).
                                                                                                                                                     OPSLIRAVENIQINEEDNEISMLQEKEREPQEV 245
                                                                                                                                                                         EMBL; U89874; AAB49491.1; -; mRNA. EMBL; Z50743; CAA90620.1; -; mRNA. PIR; S58313; SS8313. SWR; P79368; 29-161. InterPro; IPR012351; Cytokine_4_hlx. InterPro; IPR012351; Cytokine_4_hlx. InterPro; IPR012452; SCF. PANTHER; PTR11574; SCF; 1. Pfam; PF02404; SCF; 1. Cell adhesion; Glycoprotein; Growth face
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE OF 8-267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytokine 11:249-256(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25
>267
215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
TOPO_DOM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKKTQTWIITCIYLQLLLFNPLVHTQGICRNRVTDDVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------KAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 KOLKKSFKSPEPRLFTPEEPFRIFNRSIDAFKOF-VVASETSOCVVSSTLSPEKG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).
-!- SUBUNIT: Homodimer, non-covalently linked (By similarity).
-!- SUBCELLULAR LOCATION' Type I membrane protein (isoforms 1 and 2) Also exists as a secreted soluble form (isoform 1 only) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCF (Fragment).
Macaca mulatta (Rhesus macaque).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                  (Potential). (Potential). (Potential). (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BMBL; AY247403; AP03067.1; -; mRNA.
HSSP, P21583; 1SCF.
SWR; Q86419; 4-136.
GO; GO:0016020; C:membrane; IEA.
GO; GO:000113; F:stem cell factor receptor binding; IEA.
GO; GO:000115; F:cell adhesion; IEA.
InterPro; IPR003452; SCF.
Finity P702404; SCF.
Cell adhesion; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                             30149 MW; 9D9D959E4B9EC841 CRC64;
                                  Cytoplasmic (Potential).
N-linked (GlcNAc. ) (IN-linked (GlcNAc. )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.5%; Score 990.5; DB 1
74.2%; Pred. No. 8.2e-70;
ive 19; Mismatches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 AA
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238
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                                                                                                                                                                                                                                                                                                                                                                         267 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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SEQUENCE
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CARBOHYD
CARBOHYD
DISULFID
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                                                     0; Gaps
                              Query Match 59.7%; Score 754; DB 2; Length 164; Best Local Similarity 99.3%; Pred. No. 2e-51; Matches 147; Conservative 0; Mismatches 1; Indels
NON_TER 164 164
SEQÜENCE 164 AA; 18430 MW; GAFE3A568730110D CRC64;
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Search completed: February 22, 2006, 18:19:22 Job time : 127.212 secs

Sequence Sequence Sequence Sequence

Sequence Seq

Sequence Sequence Sequence Sequence

us-10-620-642-63.rai

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OM protein

Run on:

Sequence:

Minimum DB Maximum DB

Database

Searched:

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1 MKKTQTWILITCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESSES

JADRESSES MAREBAll, O'Toole, Geretein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive (TTY: Chicago STRATE: 111inois

COUNTRY: United States of America COUNTRY: United States of America (TTY: 60606-6402

COMPUTER: 111inois

COMPUTER: 111inois

COMPUTER: 11 PR PC compatible (COMPUTER: 12 PR PC COMPUTER: 12 PAPLICATION NUMBER: 12/08/482,918

FILING DATE: 07-UTN-1995

CLASSIFICATION NUMBER: 36,107

REPERENCY AGENTION HORBER: 36,107

REPERENCY AGENTION HORBER: 36,107

REPERENCY AGENTION HORBER: 36,107

REPERENCY AGENTION HORBER: 36,107

REPERENCY 10 NUMBER: 36,107

REPERENCY 11 NUMBER: 36,107

REPERENCY 12 AND NO: 63: 5EQUENCE CHARACTERISTICS: 12 AGENTION POR SEQ IN NO: 63: 12 AGENTION ACCOUNTS AND ACCOUNTS
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100.0%; Score 1262; DB 2;
Best Local Similarity 100.0%; Pred. No. 3.3e-125;
Matches 245; Conservative 0; Mismatches 0;
                                                             US-09-604-325A-48
US-09-604-325A-48
US-09-635-251-50
US-09-224-681-50
US-09-224-683-50
US-08-336-728A-50
US-08-336-728A-82
US-08-336-728A-82
US-08-955-848A-82
US-08-224-681-57
US-09-224-681-57
US-09-224-683-57
US-09-224-683-57
US-09-224-683-57
US-09-224-683-57
US-09-224-683-57
US-09-604-325A-57
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US-09-604-325A-57
US-09-604-325A-57
US-09-604-325A-57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-482-918-63; Application US/08482918; Sequence 63, Application US/08482918; Patent No. 6207417; GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.; APPLICANT: Bosselman, Robert A. APPLICANT: Bosselman, Robert A. APPLICANT: Martin, Francis H.; TITLE OF INVENTION: Stem Cell Factor; NUMBER OF SEQUENCES: 104; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-918-63
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                                                                                                                                                                                                                                        .; Search time 29.697 Seconds (without alignments) 682.074 Million cell updates/sec
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1262
1 MKKTQTWILTCIYLQLLLFN.....NBEDNEISMLQEKEREPQEV 245
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                                GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-09-224-681-63
US-09-234-681-63
US-09-635-251-63
US-09-24-683-63
US-09-949-016-9392
US-09-949-016-9392
US-08-482-918-49
US-08-482-918-49
US-08-482-918-49
US-08-224-681-61
US-09-224-681-61
US-08-336-728A-49
US-08-336-728A-61
US-09-635-251-61
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US-09-635-251-61
US-09-604-325A-61
US-09-949-016-9393
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US-09-949-016-9394
US-08-482-918-48
US-09-224-681-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 572060 segs, 82675679 residues
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                                                                                                                                                                                                                                               February 22, 2006, 18:19:42
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                          protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq length: 0
seq length: 200000000
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Match Length
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Perfect score:
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Score

Result Š. ö 9

Gaps

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Length 245;

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amino acid
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                                                                                                                                   TOPOLOGY:
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APPLICANT: Scebo, Kristina M.
APPLICANT: Scebo, Sidney V.
APPLICANT: Sugges, Sidney V.
APPLICANT: Sugges, Sidney V.
APPLICANT: Sugges, Sidney V.
APPLICANT: Sugges, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
TITLE OF INVENTION: Areas are nower, 233 South Wacker Drive
CORRESPONDENCE ADDRESS

ASTATE: Illinois
COUNTRY: United States of America
COUNTRY: United States of America
COMPUTER FADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: APPLICATION DATE:
APPLICATION NUMBER: US/09/224,681
61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                     KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKGKAKNPP 180
                                                                                             121 KOLKKSFRSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKGKAKNPP 180
                                                                                                                                                                GDSSLHWAAMALPALFSLIIGFAFGALYWKKRQPSLTRAVENIQINEEDNEISMLQEKER 240
                                                                                                                                                                                           NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION NUMBER: 07/589,701
FILING DATE: 24-AUG-1990
PRIOR APPLICATION NUMBER: 07/573,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
RATIOR ARPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 63, Application US/09224681
Patent No. 6207454
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US-09-224-681-63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 MDVLPSHCWISEMVVQLSDSLTDLLDKPSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 KOLKKSPKSPEPRLFTPEEFFRIFNRSIDAFKOFVVASETSDCVVSSTLSPEKGKAKNPP
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                                                                                                                                                                                                                                                                                                                        Gaps
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Sequence 63, Application US/08336728A;
Patent No. 6207802;
GENERAL INPORMATION:
APPLICANT: Seabo, Krisztina M.
APPLICANT: Suggs, Sidney V.
APPLICANT: Stancis H.
CORRESPONDENCES: 104
CORRESPONDENCES: 104
CORRESPONDENCES: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                         Length 245;
                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
                                                                                                                                                                                                                                                                           Score 1262; DB 2;
Pred. No. 3.3e-125;
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                                                                                                                                                                                                                                                    100.0%; Scor.
v 100.0%; Pred. No. 3...
0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION INDERS: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION NUMBER: 07/589,701
PRIOR APPLICATION NUMBER: 07/589,701
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 24-AUG-1990
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                 TELEX:
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 245; Conservative
                                                                                                                                                                                                   MOLECULE TYPE: protein
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKGKAKNPP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKKTQTWILICIYLQLLEPNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 245;
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Sequence 63, Application US/09224683
Patent No. 6441147
GENERAL INFORMATION:
APPLICANT: Zebc, Krisztina M.
APPLICANT: Sugge, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1262; DB 2;
100.0%; Pred. No. 3.3e-125;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32957A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/449,182

APPLICATION NUMBER: 08/172,329

FILING DATE: 21-DEC-1993

APPLICATION NUMBER: 07/684,535

FILING DATE: 25-NO'1992

APPLICATION NUMBER: 07/684,535

FILING DATE: 01-OCT-1991

APPLICATION NUMBER: 07/589,701

FILING DATE: 01-OCT-1990

APPLICATION NUMBER: 07/573,616

FILING DATE: 24-AUG-1990

APPLICATION NUMBER: 07/573,616

FILING DATE: 24-AUG-1990

APPLICATION NUMBER: 07/573,616

FILING DATE: 01-OCT-1990

APPLICATION NUMBER: 07/573,616

FILING DATE: 11-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 63: US-09-635-251-63
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 245 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: <UNKNOWN>
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 245; Conservative
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDLKKSPKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKGKAKNPP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKGKAKNPP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDSSLHWAAMALPALFSLIIGFAFGALYWKKRQPSLTRAVENIQINEEDNEISMLQEKER 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKKTQTWILICIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 GDSSLHWAAMALPALFSLIIGFAFGALYWKKRQPSLTRAVENIQINEEDNEISMLQEKER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 6666-6402
COMPUTER READABLE FORM:
MEDIUM TYEE: PLOPEY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRIT APPLICATION DATE: 07-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Seebo, Krisztina M.
Bosselman, Robert A.
Suggs, Sidney V.
Suggs, Sidney V.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1262; DB 2;
Pred. No. 3.3e-125;
Mismatches 0;
                                                                                                                                                                                        01017/32956
  APPLICATION NUMBER: 07/537,198
FILING DATE: 11-UUN-1990
PRIOR APPLICATION DATA: 307,422,383
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-CCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Sco-
100.0%; Pre
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Patent No. 6759215
GENERAL INFORMATION:
                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                          TELEX: 25-3856
INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS: LENGTH: 245 amino acids TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 245; Conservative
                                                                                                                                                                                                                                                        312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-336-728A-63
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US-09-635-251-63
                                                                                                                                                                                                                                                        TELEFAX:
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Gaps

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121 KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKGKAKNPP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: CILCAGO
COUNTRY: United States of America
ZIP: 6060-6402
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
APPLICATION NUMBER: 07/982, 255
FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/593, 106
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/537, 198
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/537, 198
FILING DATE: 11-JUN-1999
ATTORNEY/AGENT INFORMATION:
NAME: Cloud, DATE: 11-JUN-1999
ATTORNEY/AGENT INFORMATION:
NAME: CLOUGKET NUMBER: 36, 107
REFERENCE/DOCKET NUMBER: 317/474.64300.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                         APPLICANT: Zsebo, Krisztina M.
Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-09-604-325A-63
                                                                                                                                                                                            US-09-604-325A-63;
Sequence 63, Application US/09604325A; Patent No. 6852313; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 25-3856
INFORMATION FOR SEQ 1D NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acid
TYPE: amino acid
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TELEFAX: 312/474-0448
      241 BFQEV 245
                                                                241 BPQEV 245
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                       CITY: Chicago
STATE: Illinois
COUNTX: United States of America
COUNTX: United States of America
ZIP: 66606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: ParentIn Pecase #1.0, Version #1.30
CURARET APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01017/35136
                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION
BRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
FILING DATE: 25-NOY-1992
FILING DATE: 25-NOY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/59,701
FILING DATE: 01-0CT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/42,383
FILING DATE: 16-0CT-1989
ATOMORY/AGENT INFORMATION:
NAME: Clough, DATA in REGISTRATION NUMBER: 36,107
REGISTRATION NUMBER: 36,107
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 36,107
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
THE PROPERTY TO THE PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
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KDLKKSFKSPBPRLFTPBEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKGKAKNPP 180
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                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1262; DB 2; Length 262; 100.0%; Pred. No. 3.7e-125; Live 0; Mismatches 0; Indels 0
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MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/220,379B
FILING DATE: 28-MAR-1994
CLASSIFICATION: 435
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Sequence 2, Application US/08220379B

Sequence 2, Application US/08220379B

Patent No. 5525708

PAPLICANT: No. 5525708ka, Karl

APPLICANT: Lobell, Robert B

TITLE OP INVENTION:

NUMBER OP SEQUENCES: 7

CORRESPONDENCE ADDRESS:
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FLING DATE: 2000-10-20
PRIOR PLING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-8
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PSESSEQ for Windows Version 4.0
SEQ ID NOS 2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
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NAME: Haley Jr, James F
REGISTRATION NUBBER: 27,794
REFERENCE/DOCKET NUMBER: Cytch
TELECOMMUNICATION INFORMATION:
TELEPAX: 212-596-9000
TELEPAX: 212-596-9000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 245; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 BFQEV 245
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                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9392
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03

PRIOR PLILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOUTHARRE: FRALESC for Windows Version 4.0

SEQ ID NO 9391
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US-09-949-016-9392

Sequence 9392, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WISH HUMAN DISEASE, OF DETECTION AND USES THEREOF

FILE REPERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14
                                                                         GDSSLHWAAMALPALFSLIIGFAFGALYWKKROPSLTRAVENIQINEEDNEISMLOEKER 240
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                                                                                                         KOLKKSPRSPEPRLFTPEEPPRIFNRSIDAPKOFVVASETSOCVVSSTLSPEKGKAKNPP
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                                                                                                                                                                                                                                                                                                                                                  Sequence 9391, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 245; Conservative
                                                                                                                                                                             241 EFQEV 245
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1-248 SCF protein begins at amino acid 26; amino acid 1-25 include Met and leader sequences for membrane band form of hurecombinant SCF."
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                                                                                                                                                                                                                                                                                                                                                                                   61 MDVLPSHCWISEMVVQLSDSLTDLLDKPSNISEGLSNYSIIDKLVNIVDDLVECVKENS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 240
                                                                                                                                                                                                                                                                          1 MKKTQTWILITCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLFKDYMITLKYVPG
                                                                                                                                                                                                                                            1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                           Indels 28; Gaps
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| Sequence 49, Application US/08482918
| Sequence 49, Application US/08482918
| Patent No. 6207417
| GENERAL INFORMATION:
| APPLICANT: Suebo, Krisztina M. APPLICANT: Suego, Sidney V. APPLICANT: Suego, Sidney V. APPLICANT: Suego, Sidney V. APPLICANT: Suem Cell Factor
| TITLE OF INVENTION: Stem Cell Factor
| OUNDERSONDENCE ADDRESS: 104
| CORRESSENDENCE ADDRESS: 300 Sears Tower, 233 South Wacker Drive CITY: Chicago
| STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago
| STREET: 111inois | STREET: 6100Py disk COUNTRY: United States of America COUNTRY: United States of America STREET: READABLE FORM: MEDIUM TYPE: Floppy disk COUNTRY: UNITER Floppy disk COUNTRY: DRIADBLE FORM: MEDIUM TYPE: PROPHY 100 NUMBER: US/08/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/08/482,918 |
| PILLING DATE: 07-UTW-1995 |
| ATTORNEY/AGENT INFORMATION: | NAME: Clough, David W. REGISTRATION NUMBER: 36,107 |
| RESPERRINGE/DOCKET NUMBER: 312/474-6300 |
| TELEPHONE: 312/474-6300 |
| TELEPHONE: 312/474-6408
                                                                                                                                     97.5%; Score 1231; DB 1; Length 273;
89.4%; Pred. No. 7.5e-122;
tive 0; Mismatches 1; Indels 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213 OPSLTRAVENIQINEEDNEISMLOBKEREFOEV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 QPSLTRAVENIQINEEDNEISMLQEKEREFGEV 273
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INFORMATION FOR SEQ ID NO: 49:
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                                                                                                                                       Query Match
Best Local Similarity 89.4
Matches 244; Conservative
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          ) OTHER INFORMATION:
) OTHER INFORMATION:
) OTHER INFORMATION:
US-08-628-428-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 ------KAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAWALPALFSLIGFAFGALYWKKR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKG----- 174
                                                                                                                                                                                                                                                                                                                                                                                   1 MKKTQTWILTCIYLQLLLENPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                                                                                                                                                                                                                                                                                                                      1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                              97.5%; Score 1231; DB 1; Length 273; 89.4%; Pred. No. 7.5e-122; tive 0; Mismatches 1; Indels 2
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Patent No. 5885962
GENERAL INFORMATION:
TYPELICANT: Lu, Hsieng
TITLE OF INVENTION: SCF ANALOG COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: AMMON INC.
STREET: Labousand Oaks
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY:
STATE: CA
COUNTRY: USA
ZIUNTRY: USA
ZIUNTRY: USA
ZIUNTRY: USA
ZIUNTRY: B1320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,428
FILING DATE: 05-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KNight, Matthew W
REGISTRATION NUMBER: 36,846
REGISTRATION NUMBER: 36,846
REGISTRATION NUMBER: 36,846
REGISTRATION COKE TOUNDER: 36,846
REGISTRATION COKE TOUNDER: 36,846
REGISTRATION COKE TOUNDER: 36,846
REGISTRATION COKE SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acide
TWENGTH: 273 amino acide
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LOCATION: 1..273
OTHER INFORMATION: /note= "NOTE: Mature full length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPSLIRAVENIQINEEDNEISMLQEKEREFQEV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 OPSLTRAVENIÓINEEDNEISMLÓEKEREFÓEV 273
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                       ) NAME/KEY: cleavage site
; LOCATION: 164..165
US-08-220-379B-2
                                                                                                                                                                                                                                                                 Best Local Similarity 89.4
Matches 244; Conservative
                                                                                    MOLECULE TYPE: protein FEATURE:
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121 KOLKKSFKSPEPRLFTPEBFPRIFNRSIDAFKDFVVASBTSDCVVSSTLSPEKG----- 174
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                                                                                                                                                                       61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                    1 MKKTQTWILTCIYLQLLLPNPLVKTEGICRNRVTNNVKOVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
APPLICANT: Zeebo, Krisztina M.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                   MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVBCVKENSS
                                                                                                                                                                                                                                                                                                                                                                                                                    ------KAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois COUNTRY: United States of America 21P: 60606-6402 COMPUTER READABLE FORM:
MEDIUM TYEE: ISOPPO HISK COMPUTER: IBM PC compatible COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 OPSLTRAVENIQINBEDNEISMLOEKEREFOEV 245
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APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION TO BATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION NUMBER: 07/589,701
FILING DATE: 25-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/53,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/53,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
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US-03-224-681-49
; Sequence 49, Application US/09224681
; Patent No. 6207454
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CLASSIFICATION:
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                                                                                                                                                                                                        1 MKKTQTWILTCIYLQLLLENPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                                                                                                                            1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
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APPLICANT: Seabo, Krieztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Buggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBERS OF SEQUENCES: 104
CORRESPONDENCE ADDRESS: 104
CORRESPONDENCE ADDRESS: 300th Wacker Drive
CITT: Chicago
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITT: Chicago
STATE: Illinois
STATE: Illinois
COUNTRY: United States of America
ZIP: 6066-6402
COUNTRY: United States of America
ZIP: 6066-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Properior
COUNTRY: UNITED FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: BM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 30,107
REGISTRATION NUMBER: 36,107
REGISTRATION NUMBER: 36,107
REGISTRATION NUMBER: 312/474-6300
TELLEPHONE: 312/474-6300
TELLEPHONE: 312/474-6300
TELLEPHONE: 312/474-6306
                             Length 273;
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                     Query Match 97.5%; Score 1231; DB 2;
Best Local Similarity 89.4%; Pred. No. 7.5e-122;
Matches 244; Conservative 0; Mismatches 1;
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Patent No. 6207417
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
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MOLECULE TYPE: protein
US-08-482-918-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-482-918-61
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APPLICANT: Seebo, Krisztina M.
APPLICANT: Sugges, Sidney V.
APPLICANT: Sugges, Sidney V.
APPLICANT: Sugges, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marehall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 6060-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICANION DATA:
APPLICANTON DATA:
APPLICANTON DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
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NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEFAX: 312/474-0448
TELEFAX: 312/
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 61, Application US/09224681
Patent No. 6207454
GENERAL INFORMATION:
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US-09-224-681-49
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US-09-224-681-61
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKPSNISBGLSNYSIIDKLVNIVDDLVBCVKENSS 120
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US-08-336-728A-48
; Sequence 48, Application US/08336728A
; Patent No. 6207802
; GENERAL INFORMATION:
; APPLICANT: Suebo, Krisztina M.
APPLICANT: Sugge, Sidney V.
; APPLICANT: Sugge, Sidney V.
; APPLICANT: Sugge, Sidney V.
; TITLE OF INVENTION: Stem Cell Factor
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEGUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 97.5%; Score 1231; DB 2; Length 273; Best Local Similarity 89.4%; Pred. No. 7.5e-122; Matches 244; Conservative 0; Mismatches 1; Indels 28
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                                                                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION NUMBER: 07/589,701
PRIOR APPLICATION NUMBER: 07/589,701
PRIOR APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 07/537,198
FILING DATE: 11-UNN-1990
PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION: NAME: Clough, David W. REGISTRATION NUMBER: 36,107
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 61: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
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121 KOLKKSFEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
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STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois COUNTRY: United States of America 21P: 60606-6402 COUNTRY: United States of America 21P: 60606-6402 COMPUTER: BADABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/336,728A FLING DATE: 09-NOV-1994 CLASSIFICATION NUMBER: US/982,255 FILING DATE: 25-NOV-1992 PRIOR APPLICATION NUMBER: 07/982,255 FILING DATE: 01-OCT-1990 PRIOR APPLICATION NUMBER: 07/533,616 FILING DATE: 01-OCT-1990 PRIOR APPLICATION NUMBER: 07/533,616 FILING DATE: 1-JUN-1990 PRIOR APPLICATION NUMBER: 07/533,616 FILING DATE: 1-JUN-1990 PRIOR APPLICATION NUMBER: 07/422,383 FILING DATE: 11-JUN-1990 PRIOR APPLICATION NUMBER: 07/422,383 FILING DATE: 11-JUN-1990 PRIOR APPLICATION NUMBER: 07/422,383 FILING APPLICATION NUMBER: 312/474-6300 TELEFRAX: 11NPORMATION: TELECOMMUNICATION CONTING ACIDE TELEGIER AND ACIDE TELEGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 OPSLTRAVENIQINEEDNEISMLOEKEREFOEV 245
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HOLECULE TYPE: protein
US-08-336-728A-48
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Sequence 63, Application US/09005243
; Sequence 63, Application US/09005243
; Patent No. US20020018763A1
; GENERAL INFORMATION:
    APPLICANT: Sugge, Sidney V.
    APPLICANT: Marth, Francis H.
    TITLE OF INVENTION: Stem Cell Factor
    CORRESPONDENCES: 104
    CORRESPONDENCES: 104
    CORRESPONDENCES: 104
    CORRESPONDENCES: 104
    CORRESPONDENCES: 104
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STRET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago
    STATE: Illinois
    COUNTRY: United States of America
    COUNTRY: United States of America
    COUNTRY: United States of America
    COMPUTER READABLE FORM:
    MEDIUM TYPE: PLOSPY disk
    COMPUTER: IBM PC compatible
    COMPUTER: BAR PC compatible
    CORRENT APPLICATION DATA:
    APPLICATION DATA:
    APPLICATION DATA:
    FILING DATE: VS/09/005,243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
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1 MKKTQTWILTCIYLQLLLFN......NBEDNBISMLQEKERBFQEV 245
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US-10-124-683-63
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US-09-005-243-49
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US-10-175-608-61
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US-10-620-642-61
US-09-005-243-48
US-09-005-243-48
US-09-005-243-683-60
US-09-005-243-683-60
US-09-175-608-50
US-09-175-608-50
US-09-175-608-50
US-09-224-683-57
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Sequence 63, Application US/09224683

Sequence 63, Application US/09224683

Patent No. US20020031491A1

GENERAL INFORMATION:
APPLICANT: Boselman, Robert A. APPLICANT: Bugges, Sidney V. APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: Gi300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois
COUNTRY: United States of America
ZIP: 66606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Batelin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/224,683
FILING DATE:
FILI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 1262; DB 3; Best Local Similarity 100.0%; Pred. No. 5.6e-114; Matches 245; Conservative 0; Mismatches 0;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFRAX: 312/474-6300
TELEFRAX: 312/474-6300
TELEFRAX: 312/474-6300
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: TYPE: protein
US-09-005-243-63
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US-09-224-683-63
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                                                                                                                                                                                                                                                                     01017/35136
APPLICATION NUMBER: 0// 202, 25
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/599, 701
FILING DATE: 01-0CT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573, 616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION NUMBER: 07/537, 198
FILING DATE: 11-UUN-1990
PRIOR APPLICATION NUMBER: 07/422, 383
APPLICATION NUMBER: 07/422, 383
FILING DATE: 16-0CT-1989
ATTORREY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
RECISTRATION NUMBER: 36,107
RECISTRATION NUMBER: 36,107
RECISTRATION NUMBER: 312/474-6300
TELEFRAN: 312/474-0448
                                                                                                                                                                                                                                                                                                                                TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 245; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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Publication No. US20040247578A1
GENERAL INFORMATION:
APPLICANT: Lotze, Michael T
APPLICANT: Lotze, Michael T
APPLICANT: Lotze, Michael T
TITLE OF INVENTION: Methods And Reagents For Inducing Immunity
FILE REFERENCE: UPT-004
CURRENT APPLICATION NUMBER: US/10/688,845
CURRENT FILING DATE: 2003-10-15
PRIOR APPLICATION NUMBER: 60/418,865
PRIOR PILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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100.0%; Pred. No. 5.6e-114;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 63, Application US/10620642; Publication No. US2050080250A1; GENERLI INFORMATION: APPLICANT: Zeebo, Krisztina M.
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 245; Conservative
                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
US-10-688-845-87
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US-10-620-642-63
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                                      MCBLUM ITER: F10py G18K
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARR: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/175,608
FILING DATE: 16-Oct-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 09/635,249
FILING DATE: 07-A0G-2000
APPLICATION NUMBER: 09/486,546
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 09/172,329
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOY-1992
APPLICATION NUMBER: 07/684,535
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/684,535
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/573,616
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100.0%; Pred. No. 5.6e-114;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
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SEQUENCE CHARACTERISTICS
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Best Local Similarity
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RESULT 4 US-10-688-845-87 ; Sequence 87, Application US/10688845

EPQEV 245

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0, Gaps (0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKGKAKNPP 180
                                                                                                                                          1 MKKTQTWILICIYLQLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                                                                             1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
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FITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
CORRESPONDENCE MARBILL, O'Toole, Geratein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago
STATE: 1111nois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/10/620,642
FILING DATE: 16-Jul-2003
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/175,608
FILING DATE: 16-Oct-2002
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MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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Pred. No. 6.7e-111;
0; Mismatches 1; Indels 21
                6300 Sears Tower, 233 South Wacker Drive
                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213 OPSLTRAVENIQINEEDNEISMLQEKEREFQEV 245
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STREET: 6300
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION
RIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,198
FILING DATE: 11-UN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-UN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/527,383
FILING DATE: 16-OCT-1999
ATTORNEY AGENT INFORMATION:
NAMME: Clough, DATAI MARE: 16-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-6448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.5%;
89.4%;
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Best Local Similarity 89.4
Matches 244; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-49
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STRANDEDNESS: 811
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                            APPLICATION NUMBER: 09/486,546
FILING DATE: 07-AUG-2000
APPLICATION NUMBER: 09/486,546
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 08/172,329
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/684,535
FILING DATE: 15-NOV-1992
APPLICATION NUMBER: 07/684,535
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/639,701
FILING DATE: 10-APR-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 16-OCT-1999
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 36,107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
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Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Buggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                  APPLICATION NUMBER: 09/635,249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 245 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Matches 245; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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Gaps

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181 KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALFALFSLIGFAFGALYWKKR 240
61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                           121 KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                          KOLKKSFKSPEPRLFTPBEFFRIFNRSIDAFKDFVVASBTSDCVVSSTLSPEKG---- 174
                                                                                                                                                                                                         -----KAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 49, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
APPLICANT: Sugge, Krisztina M.
APPLICANT: Sugge, Sidney V.
APPLICANT: Sugge, Sidney V.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS: 104
CORRESPONDENCE ADDRESS: ABASEALI, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 6300 Saars Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois CUNTRY: United States of America ZIP: 6060-6402 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible SOSTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/224,683
FILING DATE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/53,616
FILING DATE: 01-OCT-1990
FILING DATE: 01-OCT-1990
FILING DATE: 01-CT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/53,198
FILING DATE: 11-UNN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATOMNEY AGENT INFORMATION:
NAME: CLOUGH, DAYIG W.
REGISTRATION NUMBER: 36,107
REBERRENCE DOCKET NUMBER: 36,107
REBERRENCE DOCKET NUMBER: 36,107
REBERRENCE DOCKET NUMBER: 36,107
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                                                                                                   Sequence 61, Application US/09005243
; Sequence 61, Application US/09005243
; Patent No. US2002018763A1
; GENERAL INPORMATION:
   APPLICANT: Zaebo, Kristtina M.
   APPLICANT: Bosselman, Robert A.
   APPLICANT: Buggs, Sidney V.
   APPLICANT: Martin, Francis H.
   TITLE OF INVENTION: Stem Cell Factor
   NUMBER OF SEQUENCES: 104
   CORRESPONDENCE ADDRESS:
   ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun STREET: Giolo Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 97.5%; Score 1231; DB 3; Length 273; Best Local Similarity 89.4%; Pred. No. 6.7e-111; Matches 244; Conservative 0; Mismatches 1; Indels 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Chicago STATE: Illinois COUNTRY: Illinois COUNTRY: Illinois COUNTRY: Illinois COUNTRY: COUNTRY: Illinois COUNTRY: COORDING COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: BATCHILIN Release #1.0, Version #1.30 SURRENT APPLICATION NUMBER: US/09/005,243
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/49,653
FILING DATE: 24-MAY-1995
CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION NUMBER: 07/59,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION NUMBER: 07/53,616
FILING DATE: 11-JUN-1990
PRIOR APPLICATION NUMBER: 07/537,198
FILING DATE: 11-OW-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REPERENCE/DOCKET NUMBER: 0101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAWALPALFSLIIGFAFGALYWKKR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                 61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDLKKSFKSPEPRLFTPBEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKG----- 174
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                                                                                                                                                                                                                                                                                                                                    1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                    28;
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Sequence 61, Application US/09224683

APPLICANT: Sebo, Kristina M.

APPLICANT: Buges, Sidney V.

APPLICANT: Buges, Sidney V.

APPLICANT: Martin, Francis H.

TITLE OF INVENTION: Stem Cell Factor: Composition Claims

NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREF: 6300 Sears Tower, 233 South Wacker Drive

COUNTRY: United States of America

COMPUTRY: United States of America

ZIP: 60606-6402

COMPUTER: IBM PC Compatible

OPERATION SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Batentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

FILING DATE:

STATE: HAND DATE:

STATE: STATE: STATE:

MEDIUM TYPE: Ploppy disk

COMPUTER: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/224,683
                                                                                                                                                                                                                                     97.5%; Score 1231; DB 3; Length 273; 89.4%; Pred. No. 6.7e-111; ive 0; Mismatches 1; Indels 2
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APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-49
                                                                                                                                                                                                                                                                                    Matches 244; Conservative
                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175
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Best Local
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28; Gaps
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Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1231; DB 3; Length 273;
Pred. No. 6.7e-111;
0; Mismatches 1; Indels 28
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STATE: Illinois
COUNTRX: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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PALOK AFFLICATION NUMBER: 07/589,701
PRIOR AFFLICATION NUMBER: 07/589,701
PRIOR AFPLICATION DATA:
APPLICATION NUMBER: 07/573,616
PRIOR AFPLICATION DATA:
APPLICATION NUMBER: 07/573,198
PILING DATE: 11-JUN-1990
PRIOR AFPLICATION DATA:
APPLICATION NUMBER: 07/422,383
PILING DATE: 11-JUN-1990
PRIOR AFPLICATION DATA:
APPLICATION NUMBER: 07/422,383
PILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, DATA:
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 36,107
TELECOMMUNICATION INFORMATION:
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US-10-175-608-49
Sequence 49, Application US/10175608
Publication No. US20040181044A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 61:
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89.4%;
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LENGTH: 273 amino acids
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Best Local Similarity 89.4
Matches 244; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-09-224-683-61
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Gerstein, Murray & Borun South Wacker Drive

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STATE: Illinois
COUNTRY: United States of America
                                                                       Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                          ADDRESSEE: Marshall, O'Toole,
STREET: 6300 Sears Tower, 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
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Best Local Similarity
    GENERAL INFORMATION
APPLICANT: Zsel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MKKTQTWILICIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1231; DB 4;
Pred. No. 6.7e-111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QPSLTRAVENIQINEEDNEISMLQEKEREFQEV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                     CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/10/175,608
FILING DATE: 16-Oct-2002
CLASSIPICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                    FILING DATE: 10-APR-1991
APPLICATION WUMBER: 09/589,701
ELING DATE: 10-0CT-1991
APPLICATION NUMBER: 07/573,616
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SEQUENCE DESCRIPTION: SEQ ID NO: 49:
                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/635, 249
                                                                                                                                                                          FILING DATE: 07-AUG-2000
APPLICATION NUMBER: 09/486,546
ELING DATE: 24-MAY-1995
APPLICATION NUMBER: 08/172,329
                                                                                                                                                                                                                                                        FILING DATE: 21-DEC-1993
APPLICATION WUMBER: 07/982,255
FILING DATE: 25-NOV-1992
APPLICATION NUMBER: 07/684,535
                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/537,198
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 11-JUN-1990
APPLICATION WINGBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 273 amino acida
TYPE: amino acid
STRANDEDNESS: single
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al Similarity 89.4%;
244; Conservative
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Best Local Similarity
Matches 244; Conserva
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MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/175,608
FILING DATE: 16-Oct-2002
CLASSIFICATION: Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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Pred. No. 6.7e-111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 61:
                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/635,249
                                                                                                                                                                                                                                                                                                    FILING DATE: 07-AUG-2000
PAPLICATION NUMBER: 09/486,546
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 08/172,329
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APPLICATION NUMBER: 07/982,255
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APPLICATION NUMBER: 07/684,535
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APPLICATION NUMBER: 09/589,701
FILING DATE: 10-OCT-1991
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FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-UUN-1990
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FILING DATE: 16-OCT-1989
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REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 010
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Sequence 61, Application US/10175608 Publication No. US20040181044A1

RESULT 11 US-10-175-608-61

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Similarity
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Best Local Simil
Matches 244; C
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US-10-620-642-61
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121 KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                               -----KAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: CALGAGO
STARET: S.100 SAGIB TOWER, 233 SOUTH WACKET DITYOR
COUNTRY: United States of America
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/620,642
FILING DATE: 16-Jul-2003
CLASS!FICATION NUMBER: US/10/15,608
FILING DATE: 16-OCT-2002
APPLICATION NUMBER: 09/635,249
FILING DATE: 07-MG-2000
APPLICATION NUMBER: 09/635,249
FILING DATE: 21-DCC-1993
APPLICATION NUMBER: 09/635,265
FILING DATE: 21-DCC-1993
APPLICATION NUMBER: 07/982,255
FILING DATE: 10-AR-1991
APPLICATION NUMBER: 07/64,535
FILING DATE: 10-AR-1991
APPLICATION NUMBER: 07/637,198
FILING DATE: 10-AR-1991
APPLICATION NUMBER: 07/537,198
FILING DATE: 10-CT-1999
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-UN-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 10-OCT-1999
ATTORNEY/AGANTION:
NAME: Clough, David W:
REGISTRATION NUMBER: 31,107
REFERENCE/DOCKET NUMBER: 31,107
REFERENCE/DOCKET NUMBER: 31,107
REFERENCE/DOCKET NUMBER: 31,107
FELECOMMUNICATION NUMBER: 31,107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                              213 QPSLTRAVENIQINEEDNEISMLQEKEREFQEV 245
                                                                                                                                                                    APPLICANT: Zeebo, Krisztina M.
Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTON: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                             Sequence 49, Application US/10620642 Publication No. US20050080250A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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US-10-620-642-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----KAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
                                                                                                                                                  Gaps
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Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                  28;
                                                                                                Length 273;
                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version #1.30
                                                                                                Score 1231; DB 5;
Pred. No. 6.7e-111;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 OPSLTRAVENIQINEEDNEISMLQEKEREFQEV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 QPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Chicago
STATE: 1111nois
COMPUTRY: United States of America
COMPUTRY: United States of America
ZIP: 6660-6402
COMPUTRY: United States of America
ZIP: 6660-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTRE: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: PATENTING NATA:
APPLICATION NUMBER: US/10/620,642
FILING DATE: 16-U1-2003
CLASSIFICATION NUMBER: US/10/175,608
FILING DATE: 16-Oct-2002
APPLICATION NUMBER: 09/635,249
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 08/172,329
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/582,255
FILING DATE: 25-MOY-1992
APPLICATION NUMBER: 07/584,535
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-620-642-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 61, Application US/10620642; Publication No. US20050080250A1; GENERAL INFORMATION: APPLICANT: Zsebo, Krisztina M.
                                                                                                   97.5%;
ilarity 89.4%;
Conservative
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Sequence 48, Application US/09005243

Patent No. US2002001863A1

GENERAL INPORATION:

APPLICANT: Saebo, Krisztina M.

APPLICANT: Bosselman, Robert A.

APPLICANT: Busselman, Robert A.

CORRESPONDERS:

ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun STREF: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

COMPUTER: EADABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: PatentIn Release #1.0, Version #1.30

CURRENTING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version BAPLICATION NUMBER: US/09/005,243

FILING DATE:

CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 97.5%; Score 1231; DB 5; Length 273; Best Local Similarity 89.4%; Pred. No. 6.7e-111; Matches 244; Conservative 0; Mismatches 1; Indels 2:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELERAX: 312/474-6300
TELERAX: 312/474-6300
TELERAX: 312/474-6300
TELERX: <UNKNOWN>
INFORMATION FOR SEQ ID NO: 61:
SEQUENCY CHARACTERISTICS:
LENGTH: 273 amino acide
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 61:
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1 MKKTQFWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKXVPG 60
1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKXVPG 60
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Sequence 48, Application US/09224683

Sequence 48, Application US/09224683

Sequence 48, Application US/0924683

Septent No. US20020013491A1

APPLICANT: Zsebo, Krisztina M.

APPLICANT: Bosselman, Robert A.

APPLICANT: Bosselman, Robert A.

APPLICANT: Martin, Francis H.

TITLE OF INVENTION: Stem Cell Factor: Composition Claims

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 QPSLTRAVENIQINEEDNEISMLQEKEREFGEV 273
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PILING DATE:

PILING DATE:

APPLICATION 1995

CLASSIPICATION DATA:

APPLICATION NUMBER: 07/982,255

FILING DATE: 25-NOV-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/589,701

FILING DATE: 25-NOV-1992

PRIOR APPLICATION NUMBER: 07/573,616

FILING DATE: 10-OCT-1990

PRIOR APPLICATION NUMBER: 07/573,198

FILING DATE: 11-JUN-1990

PRIOR APPLICATION NUMBER: 07/573,198

FILING DATE: 16-OCT-1989

ATTORNEY/AGENT INFORMATION:

NAME: Cloudy, DATA:

APPLICATION NUMBER: 36,107

REFERENCE/DOCKET NUMBER: 36,107

REFERENCE/DOCKET NUMBER: 312/474-6300

TELEPHONE: 312/474-6300

TELERY: 25-3856

INPORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERIFICS:

LENGTH: 273 amino acids

TYPE: AMINO acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 89.0
Matches 243; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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US-09-005-243-48
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20年の大学の大学の大学を表現である。

Search completed: February 22, 2006, 18:26:56 Job time : 98.865 secs

5222, 5224, 5228, 5230, 5334, 5230, 5200, 5211, 5211,

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BOSSELMENT ROBERT A.

Suggs, Sidney V.

Martin, Francis H.

TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESCEE Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: 1111nois
COUNTRY: United States of America
COUNTRY: United States of America
COUNTRY: United States of America
COUNTRY: BAP PC Compatible
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BAP PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION AUGHORN: <a href="https://doi.org/10/353/783">CLASSIFICATION: <a href="https://doi.org/10/353/783">doi.org/10/353/783</a>
FILING DATE: 28-Jan-2003
CLASSIFICATION: <a href="https://doi.org/10/353/783">doi.org/10/353/783</a>
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US-11-176-830-510

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US-11-176-830-514

US-11-176-830-522

US-11-176-830-524

US-11-176-830-531

US-11-176-830-531

US-11-176-830-531

US-11-176-830-531

US-11-176-830-540

US-11-176-830-540

US-11-176-830-507

US-11-176-830-507

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US-11-176-830-507

US-11-176-830-507

US-11-176-830-511

US-11-176-830-515

US-11-176-830-515

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1
US-10-353-783-63
Sequence 63, Application US/10353783
Sequence 63, Application Wo. US20050261175A1
Dublication No. US20050261175A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Kristina M.
Bosselman, Robert A.
Bosselman, Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Clough, David W. REGISTRATION NUMBER: 36,107
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     February 22, 2006, 18:22:17; Search time 9.44904 Seconds (without alignments) 386.005 Million cell updates/sec
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1262
1 MKKTQTWILTCIYLQLLLFN......NBEDNBISMLQBKBRBFQEV
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US-10-353-783-69
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US-10-519-390-24
US-11-176-830-520
US-11-176-830-529
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
                     GenCore (c) 1993 .
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length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published
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Bed Bed

Minimum DB Maximum DB

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Perfect score:

Sequence:

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Scoring table:

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121 KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKG----- 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
US-10-353-783-61
is Sequence 61, Application US/10353783
is Sequence 61, Application US/10353783
is Sequence 61, Application No. US20050261175A1
is CHORNATION:
Bublication No. US20050261175A1
is CAPITICANT: Zeebo, Krisatina M.
Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
INUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
INTERT: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STREET: 6300 Sears Tower, 233 South Wacker Drive
COUNTRY: United States of America
STATE: 111inois
COUNTRY: United States of America
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 273;
           APPLICATION NUMBER: 07/589,701
FILING DATE: 01-0CT-1990
APPLICATION NUMBER: 07/53,616
FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-0TN-1990
APPLICATION NUMBER: 07/42,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 97.5%; Score 1231; DB 6;
Best Local Similarity 89.4%; Pred. No. 1.3e-105;
Matches 244; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPSLIRAVENIQINEEDNEISMLOEKEREFOEV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 QPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 49:
15-10-353-783-49
                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 273 amino acids
                                                                                                                                                                                                                                                                                                                                                    TELEX: <UNKNOWN>
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKGKAKNPP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDSSLHWAAMALPALFSLIIGFAFGALYWKKROPSLTRAVENIOINEEDNEISMLOEKER
                                                                                                                                                                                                                                                                                                                                    Gaps
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US-10-353-783-49

i Sequence 49, Application US/10353783

i Publication No. US20050261175A1

GENERAL INFORMATION:

APPLICANT: Zeebo, Krisztina M.

BOSSElman, Robert A.

Suggs, Sidney V.

MATTIN, Francis H.

TITLE OF INVENTION: Stem Cell Factor

NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Boru

STEET: GAOGO Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 1262; DB 6; Length 245; Best Local Similarity 100.0%; Pred. No. 1.7e-108; Matches 245; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Chicago
STATE: 11linois
CONTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APELICATION DATA:
APPLICATION NUMBER: US/10/353,783
FILING DATE: 24-An-2003
CLASSIFTCATION NUMBER: 08/448,729
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 08/172,329
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
APPLICATION NUMBER: 07/684,535
                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-10-353-783-63
                TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acids
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EFOEV 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                        Version #1.30
                                                                        PRIOR DATE: 28-Jan-2003

CLASSIFICATION NAMER: 08/448,729

PRIOR APPLICATION: cUnknown>
PRIOR APPLICATION NAME: 08/448,729

FILING DATE: 21-DEC-1993

APPLICATION NUMBER: 07/982,255

FILING DATE: 21-DEC-1993

APPLICATION NUMBER: 07/82,255

FILING DATE: 21-DEC-1993

APPLICATION NUMBER: 07/84,535

FILING DATE: 10-APR-1991

APPLICATION NUMBER: 07/89,701

FILING DATE: 10-CCT-1990

APPLICATION NUMBER: 07/89,7198

FILING DATE: 11-TUN-1990

APPLICATION NUMBER: 07/82,383

FILING DATE: 11-TUN-1990

APPLICATION NUMBER: 07/422,383

TELEGRAX: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 97.5%; Score 1231; DB 6; Best Local Similarity 89.4%; Pred. No. 1.3e-105; Matches 244; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPSLTRAVENIOINEEDNEISMLOEKEREFOEV 245
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/353,783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 61:
US-10-353-783-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 48, Application US/10353783
Publication No. US20050261175A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
Bosselman, Robert A.
Suggs, Sidney V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
US-10-353-783-48
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-----KAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                               ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 273;
                                                                                            STREET: 6300 Sears Tower, 233 SOUTH WACKET DITUE
CUTYX: CLALGAGO
STATE: Illinois
COMPUTRY: United States of America
ZIP: 6606-6402
COMPUTRY: Indied States of America
ZIP: 6606-6402
COMPUTER: IBM PORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM POLICATION DATA:
COMPUTR: Data tentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/353,783
FILING DATE: 28-Jan-2003
CLASSIFICATION NUMBER: 08/448,729
FILING DATE: 21-DEC-1992
APPLICATION NUMBER: 07/684,535
FILING DATE: 10-ART-1992
APPLICATION NUMBER: 07/689,701
FILING DATE: 10-ART-1990
APPLICATION NUMBER: 07/53,616
FILING DATE: 10-ART-1990
APPLICATION NUMBER: 07/53,198
FILING DATE: 10-OCT-1990
APPLICATION NUMBER: 07/53,198
FILING DATE: 10-OCT-1990
APPLICATION NUMBER: 07/53,198
FILING DATE: 10-OCT-1989
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 01017/32958A
TELERPAX: 312/474-6300
TELERPAX: 312/474-6308
TELERPAX: 312/474-6308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 97.1%; Score 1226; DB 6; Best Local Similarity 89.0%; Pred. No. 3.8e-105; Matches 243; Conservative 0; Mismatches 2;
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 48: US-10-353-783-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: 111inois COUNTRY: United States of America ZIP: 6606-6402 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPUTELABLE OF COMPUTER: DAY PC COMPUTELABLE OF SYSTEM: PC COMPUTER DAY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 273;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32958A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                         241 ÓPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/353,783
FILING DATE: 28-Jan-2003
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/448,729
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
APPLICATION NUMBER: 07/684,535
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/589,701
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/589,701
FILING DATE: 10-OCT-1990
APPLICATION NUMBER: 07/53,616
FILING DATE: 11-UN-1990
APPLICATION NUMBER: 07/53,198
FILING DATE: 11-UN-1990
APPLICATION NUMBER: 07/53,198
FILING DATE: 11-UN-1990
APPLICATION NUMBER: 07/52,383
FILING DATE: 11-UN-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 11-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 50: US-10-353-783-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Zsebo, Krisztina M.
                                                                                                                                                                                                                                                                                                                                                       Sequence 50, Application US/10353783 Publication No. US20050261175A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 273 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                  US-10-353-783-50
213
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1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLFKDYMITLKYVPG

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JOHNSTAIL INFOGRATION:

JAPPLICANT: HEDEXGEN Inc.

JAPPLICANT: CHUNG, Yong-Hoon

JAPPLICANT: LEB. Hak-sup

JAPPLICANT: ILE, Hak-sup

JAPPLICANT: KIM, Jae-Youn

JAPPLICANT: KIM, Jae-Youn

JAPPLICANT: KIM, Jae-Youn

JAPPLICANT: HEO, Youn-Hwa

JITILE OF INVENTION: A method of improving efficacy of biological response-modifying

JITILE OF INVENTION: A method of improving efficacy of biological response-modifying

JITILE OF INVENTION: A method of improving efficacy of biological response-modifying

JUNERNI APPLICATION NUMBER: US/10/519,390

CURRENT APPLICATION NUMBER: XR10-203-0051846

PRIOR FILING DATE: 2003-07-26

SOFTWARE: Kopatentin 1.71

SEQ ID NO 24

LENGTH: 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: SCF: 63rd, 102nd, 110th, 115th, 116th, 119th, 126th, 129th, ; OTHER INFORMATION: 158th, 199th, 205th, 207th or 245th Phe is replaced by Val. US-10-519-390-24
                                                                                                                                                121 KOLKKSFKSPEPRLFTPEEFPRIFNRSIDAFKDFAVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                        212
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                                                              61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                                         121 KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EGICRNRVTNNVXDVTKLVANLPKDYMITLKYVPGMDVLPSHCWISEMVVQLSDSLTDLL
1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                           MDVLPSHCWISEMVVQLSDSLTDLLDXFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RSIDAFKDFVVASETSDCVVSSTLSPEKG------
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                                                                                                                                                                                                                                                                                        OPSLTRAVENIQINEEDNEISMLOEKEREFOEV
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 24, Application US/10519390; Publication No. US20060008872A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245
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Sequence 537, Application US/11176830

Sequence 537, Application US/11176830

Publication No. US20060020116A1

GENERAL INFORMATION:
APPLICANT: Gantier, Rene
APPLICANT: Gantier, Rene
APPLICANT: Object Manuel
APPLICANT: Vega, Manuel
APPLICANT: Vega
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 DKPSNISEGLSNYSIIDKLVNIVDDLVECVKENSSKDIKKSFKSPEPRLFTPEEFFRIFN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSSKDLKKSFKSPERPRLFTPEBFFRIFN 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 BGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPGMDVLPSHCWISEMVVQLSDSLTDLL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28;
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Best Local Similarity 87.9%; Pred. No. 2.2e-93;
Matches 218; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                  86.9%; Score 1097; DB 7;
87.9%; Pred. No. 2.2e-93;
rative 1; Mismatches 1;
PRIOR FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: 60/409,898
PRIOR FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: PASISEQ for Windows Version 4.0
SEQ ID NO 520
LENGTH: 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 218; Conservative
                                                                                                                                                                                                                                                      TYPE: PRT
GRGANISM: Homo sapiens
US-11-176-830-520
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US-11-176-830-537
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241 KEREFQEV 248
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Best Local Similarity
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                                                 Sequence 206, Application US/11176830

Sequence 206, Application US/11176830

Publication No. US20060020116A1

GENERAL INFORMATION:

APPLICANT: Gantier, Rene

APPLICANT: Gantier, Lila

APPLICANT: Cantier, Lila

APPLICANT: Drittanti, Lila

APPLICANT: Drittanti, Lila

APPLICANT: Drittanti, Lila

APPLICANT: Vega, Manuel

ITILE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding NU

TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding NU

TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding NU

TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding NU

TITLE OF INVENTION: Rational Evolution Related Applications

FILE OF INVENTION NUMBER: US/11/176,830

CURRENT APPLICATION NUMBER: US/11/176,834

PRIOR PILING DATE: 2003-09-09

PRIOR PILING DATE: 2003-09-09

NUMBER OF EGO ID NOS: 1306

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 206

LENGTH: 248
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SEQUENCE 520, Application US/11176830
Publication No. US20060020116A1
GENERAL INFORMATION:
APPLICANT: Gantier, Rene
APPLICANT: Guyon, Thierry
APPLICANT: Usea, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
TITLE OF INVENTION: Rational Bvolution of Cytokines for Higher Stability, Encoding Nu
TITLE OF INVENTION: Rational Bvolution of Cytokines for Higher Stability, Encoding Nu
TITLE OF INVENTION: Rational Bvolution of Cytokines for Higher Stability, Encoding Nu
TITLE OF INVENTION: 1006cules and Related Applications
TITLE OF INVENTION NUMBER: US/11/176,830
CURRENT APPLICATION NUMBER: US/68,834
PRIOR FILING DATE: 2003-09-08
PRIOR APPLICATION NUMBER: 60/457,135
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87.1%; Score 1099; DB 7; Length 248;
Best Local Similarity 88.3%; Pred. No. 1.5e-93;
Matches 219; Conservative 0; Mismatches 1; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OKGANISM: Homo sapiens

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: Genbank AAA85450

;; DATABASE ENTRY DATE: 1996-01-19

US-11-176-830-206
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US-11-176-830-520
                                  -11-176-830-206
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; ORGANISM: Homo sapiens
US-11-176-830-529
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| Sequence 519, Application US/11176830
| Publication No. US20060020116A1
| GENERAL INFORMATION:
| APPLICANT: Gantier, Rene
| APPLICANT: Guyon, Thierry
| APPLICANT: Use, Manuel
| TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu TITLE OF INVENTION: NUMBER: 10/658,834
| PRIOR PLING DATE: 2005-07-06
| PRIOR PAPLICATION NUMBER: 60/457,135
| PRIOR PALING DATE: 2003-09-09
| NUMBER OF SEQ ID NOS: 1306
| SEQ ID NO 519
| LENGTH: 248
| LENGTH: 248
| LENGTH: 248
                                                                                                                           DKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSSKDLKKSFKSPEPRLFTPEEFFRIFN 145
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                                                         RSIDAFKDFVVASETSDCVVSSTLSPEKG-
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05-11-17-6330-529
; Sequence 529, Application US/11176830
; Publication No. US20060020116A1
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APPLICANT: Gantier, Rene
APPLICANT: Guyon, Thierry
APPLICANT: Guyon, Thierry
APPLICANT: Guyon, Thierry
APPLICANT: Drittanti, Lila
APPLICANT: Usea, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu;
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu;
TITLE OF INVENTION: Acid Molecules and Related Applications
FILE REFERENCE: 17109-012002 (9228)
CURRENT PILING DATE: 2003-09-08
FRIOR PILING DATE: 2003-09-08
FRIOR PILING DATE: 2003-03-21
FRIOR PILING DATE: 2002-09-09
FRIOR PILING DATE: 2002-09-09
FRIOR PILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 529
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Sequence 536, Application US/11176830

Publication No. US20060020116A1

GENERAL INFORMATION:

APPLICANT: Gurantier, Rene

APPLICANT: Guyon, Thierry

APPLICANT: Drittanti, Lila

APPLICANT: Vega, Manuel

TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu.

TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu.

TITLE OF INVENTION: Acid Molecules and Related Applications

FILE REPREMENT: 1005-07-06

CURRENT FILING DATE: 2003-07-06

PRIOR PILING DATE: 2003-03-09

PRIOR PILING DATE: 2003-03-09

PRIOR APPLICATION NUMBER: 60/457,135

PRIOR APPLICATION NUMBER: 60/457,135

PRIOR APPLICATION NUMBER: 60/459,898

PRIOR PILING DATE: 2003-09-09

NUMBER OF SEQ ID NOS: 1306

SEQ ID NO 536

LENGTH: 248
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Best Local Similarity 87.9%; Pred. No. 2.7e-93;
Matches 218; Conservative 1; Mismatches 1;
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CREATE APPLICATION WIGHER OF SEQUENCE OF S
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Publication No. US20060020116A1

GENERAL INFORMATION:
APPLICANT: Gantier, Rene
APPLICANT: Guyon, Thierry
APPLICANT: Drittanti, Lila
APPLICANT: Vega, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding No. 11TLE OF INVENTION: Acid Molecules and Related Applications
61 DKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSSKOLKKSFKSPEPRLFTPEEPFRIFN 120
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ORGANISM: Homo sapiens
                                                                                                                KEREFOEV 245
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US-11-176-830-500
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Publication No. US20060020116A1

GENERAL INFORMATION:

APPLICANT: Gantier, Rene

APPLICANT: Guyon, Thierry

APPLICANT: Usery

APPLICANT: Vega, Manuel

ITILE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu TITLE OF INVENTION: Acid Molecules and Related Applications

ITILE OF INVENTION: Acid Molecules and Related Applications

ITILE OF INVENTION: Acid Molecules and Related Applications

ITILE OF INVENTION: Acid Molecules and Related Applications

CURRENT APPLICATION NUMBER: US/11/176,830

CURRENT PILING DATE: 2003-09-06

PRIOR PILING DATE: 2003-09-06

PRIOR PELICATION NUMBER: 60/457,135

PRIOR APPLICATION NUMBER: 60/457,135

PRIOR APPLICATION NUMBER: 60/409,898

PRIOR PILING DATE: 2002-09-09

NUMBER OF SEQ ID NOS: 1306

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 538

LENGTH: 248
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                                                                                                                Length 248;
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                                                                                                             Score 1096; DB 7;
Pred. No. 2.7e-93;
1; Mismatches 1;
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Best Local Similarity 87.9%; Pred. No. 2.7e-93;
Matches 218; Conservative 1; Mismatches 1;
                                                                                                             Query Match 86.8%;
Best Local Similarity 87.9%;
Matches 218; Conservative
                        ; ORGANISM: Homo sapiens
US-11-176-830-536
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US-11-176-830-538
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US-11-176-830-538
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FILE REFERENCE: 17109-012002 (922B)

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RSIDAFKDFVVASETSDCVVSSTLSPEKG--------KAK 177
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CURRENT APPLICATION NUMBER: US/11/176,830
CURRENT FILING DATE: 2005-07-06
PRIOR PILING DATE: 2005-07-08
PRIOR FILING DATE: 2003-09-08
PRIOR FILING DATE: 2003-03-21
PRIOR PILING DATE: 2003-03-21
PRIOR PILING DATE: 2003-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: PSESEQ for Windows Version 4.0
SEQ ID NO 500
LENGTH: 248
                                                                                                                                                                                    TYPE: PRT
CORGANISM: Homo sapiens
US-11-176-830-500
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KEREFQEV 248
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Search completed: February 22, 2006, 18:27:29 Job time : 10.449 secs